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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Geogawa and mananogaster BAC library was prepared by Kazucoyo Geogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digettion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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0
                                                                                       Length 1675;
                                                                                       Score 95.4; DB 9; Length 1
Pred. No. 7.3e-08;
0; Mismatches 189; Indels
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                                                                                           Query Match 24.0%;
Best Local Similarity 51.9%;
Matches 204; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1146)

2 NIH-MGC http://mgc.nci.nih.gov/

2 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Unpublished (1999)

2 Unpublished (1999)

3 Tissue Procurement: ATCC

3 CONA Library Preparation: Rubin Laboratory

4 CONA Library Preparation: Rubin Laboratory

5 CONA Library Preparation: Rubin Laboratory

5 CONA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

5 DNA Sequencing by: Agencourt Bioscience Corporation

7 Clond through the 1.M.A.G.E. Consortium/LLNL at:

6 Http://mage.llnl.gov

7 Column: 02

7 High quality sequence stop: 163

8 Location/Qualifiers

7 Column: 02

7 Location/Qualifiers

7 Column: 02

8 Location/Qualifiers

8 Consortium/LLNL at:

8 Column: 02

9 Location/Qualifiers

8 Column: 02
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Homo sapiens cDNA clone
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                                                                                                                                                                                                                           874 SCSCGCCSCGCGCSCCCGGCGCSGSSSGCGCCCCGGCCGGSCGCCCSSCC 815
                                                                                                                                                                                                                                                                                              157 Acgregoegagegacregogaccegecaccegrecregecerreaccrrecagerecee 216
                                                                                                                                                                                                                                                                                                                           814 GCGCCGSCSCGCCCGGCSGGCCGSSGCGGSGCCGSSCCGCSGSKCCGCGGG 755
                                                                                                                                                                                                                                                                                                                                                                                           97 CGGGGCCAGGCCGCGCTCCCAGTGGATTCGCGGGCACAGACGCCCCAGGACCGCGTTCCC 156
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     Length 935;
Query Match
22.9%; Score 90.8; DB 9; Length 9
Best Local Similarity 35.6%; Pred. No. 5.4e-07;
Matches 116; Conservative 84; Mismatches 126; Indels
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Similarity
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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IMAGE:1155002 5', mRNA Bequence.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NOI-CGBP clone distribution information can http://image.llni.gov

http://image.llni.gov

Plate: LLAM1183 row: m column: 19

High quality sequence stop: 263.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 TTCAGGCAGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCCGC 396
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                    CGTGGCGGAGGGACTGGGGACCCGGCCACCGTCCTGCCCCTTCACCTTCCAGCTCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                            218 TCCTCCGCGCGGACCCCGCCCCGTCCCGACCCCTCCCGGGTCCCCCGGCCCCAGCCCCTCC
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Amphibia, Renopus, Xenopus, Xenopus,
1 (bases 1 to 1020)
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                                                                                                                                                                  22.9%; Score 90.8; DB 5; Length 1146; 49.9%; Pred. No. 5.3e-07; ative 0; Mismatches 180; Indels 0;
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/mol_type="mRNA"
/db_xref="taxon:8355"
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                                                                                                                                                                                   Best Local Similarity 49.9
Matches 179; Conservative
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/tissue_type="embryo (stage 10)"
| Tab host="DH10B (phage-resistant)" |
|/clone lib="NH10B (phage-resistant)" |
|/clone lib="NH1D XGC Embl" |
|/note="Vector: pcMv-SFORT6; Site_1: NotI; Site_2: SalI; |
|/note="Vector: pcMv-SFORT6; Site_1: NotI; Site_2: SalI; |
|/cloned unidirectionally. Primer: Oligo dr. Average insert size l. S. kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
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S, mRNA Bequence.
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I (bases 1 to 967)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2427 row: e column: 05
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Pred. No. 6.3e-07;
0; Mismatches 196; Indels
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50.0%;
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Similarity
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           /clone="IMAGE:626404"
/tissue_type="melanotic melanoma, cell line"
/tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_112"
/note="Organ: BKin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: BKin; Vector: poTB7; Site_1: XhoI; Site_2: 
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AGENCOURT 8818583 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6390550
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MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Sugan L. Sullivan, PhD.
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Best Local Similarity 49.2%; Pred. No. 2.1e-06;
Matches 183; Conservative 0; Mismatches 189; Indels
xref="taxon:9606"
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SM Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae,
Mammalla; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae, Mus.

E 1 (bases 1 to 944)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.4.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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AGENCOURT 10137554 NIH MGC 134 Mus musculus CDNA clone
INAGE:6512731 5', mRNA sequence.
BUS16035.1 GI:228233561
                                                                                                                                           /mol_type="mRNA"
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//note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
By ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."
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23
   Plate: LLAM13877 row: f column:
                                                                                                                  /organism="Mus musculus"
                           High quality sequence stop: 554
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
   Smail: cgapbs-r@mail.nih.gov
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                                                                                                                    /mol_type="mRNA"
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/db_xref="taxon:10090"
/clone=!mAGE:6512731"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 134"
/note="Vector: pCWV-SPORT6.1; Site 1: EcoRV; Site 2: Not1;
/lone unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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Xenopus tropicalis
Eukaryotas
Eukaryotas
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases 1 to 807)
II (bases 1 to 807)
II Mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT_14925914 NICHD_XGC_Emb7 Xenopus tropicalis cDNA clone
IMAGE:6978819 5', mRNA sequence.
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14085 row: e column: 20
High quality sequence stop: 324.
Location/Qualifiers
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                                                                                      1. .944
/organism="Mus musculus"
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Matches 185; Conservative
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AGENCOURT_8968082 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491334
5', mENA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lette; //image.lln.gov
Dlate: LibM14635 row: n column: 02
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High quality sequence estart: 6
High quality sequence stop: 232.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutherlia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 972)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                         /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert aize 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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http://image.llnl.gov
plate: LLAMA4042 row: j column: 07
High quality sequence stop: 430.
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                                                                                                                                                                                           /organism="Mus musculus"
/mol type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491334"
 Email: cgapbs-r@mail.nih.gov
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/organism="Mus musculus"
//organism="mkna"
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ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                  Ph.D. corp Library Preparation: ResGen, Invitrogen Corp CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: found through the I.M.A.G.E. consortium/LLNL at: ILAMI1791 row: o column: 13 High quality sequence stop: 413.
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Cmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                           Direct Submission of the Standard Sequences of Submisted (02-JUN-1999) Genoscope - Centre National de Sequences : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Erosophila DNA provided by the BDGP from the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allensessions@syngenta.com
BMBI: allens.sessions@syngenta.com
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
class: TDNA tagged.
Location/Qualifiers
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1 (bases 1 to 982)
Sessions. A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Dietrich, B., Hor, B., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mizal, T., Kategiri, F., Clazebrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
Plant (12), 2985-2994 (2002)
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/db xref="taxon:3702"
/clone="SAIL_207_809.v1"
/clone="SAIL_207_809.v1"
/clone lib="SAIL_Collection"
/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phtp://image.llnl.gov
Rlate: LLAM12873 row: m column: 11
High quality sequence stop: 397.
Location/Qualifiers
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                                                                                           NIT WOCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRX cedex - FRANCE (E-mail: seqref@genoscope.cne.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a WRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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(organ="brosophila melanogaster" / organ="brosophila melanogaster" / ob_xref="taxon:7227" / olone="backgrosophila" / olone lib="brossac" / plasmīd="pselogac"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1088)

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
labete: LLAM14047 row: m column: 06
High quality sequence stop: 116.
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/mol_type="mRNA"
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/clone="texon:10000"
/tissue_type="retina"
/lab_host="bH108 (phsge-resistant)"
/clone_lib="NIH_MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3:3 kb. Library enriched for
full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Copyright (c) 1993 - 2005 Compugen Ltd.
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	Description	Sequence 93, Appl	Sequence	Sequence 6, Appli	Sequence 1	Sequence 1	Sequence	Sequence 1, Appli	Sequence 1	Sequence	Seguence
SUMMARIES	ID	US-10-081-969-93	3 US-10-456-830-1	US-10-325-810-6	US-09-783-203-1	US-09-994-427A-1	US-09-995-419A-1	US-10-141-220-1	US-10-023-969-1	US-10-206-447-1	US-10-674-836-1
	Query Score Match Length DB I	397 15	4293 18	Н	σ	σ	Ä	Ä	Ä	Ä	H
di	Query Match Le	100.0	100.0								
	Score	397	397	397	397	397	397	397	397	397	397
	Result No.	-	~	e	4	S	9	7	8	6	10

	Sequence 144, Apple Sequence 144, Apple Sequence 24, Appli Sequence 24, Apple Sequence 24, Apple Sequence 25, Apple Sequence 25, Apple Sequence 25, Apple Sequence 26, Apple Sequence 17, Apple Sequence 11, Apple Sequence 21, Apple 21, App	denoviral Vectors
9. US-10. 840-455-3 9. US-10. 840-455-43 10. US-09-733-2244A-30 10. US-09-956-335-1 10. US-09-956-335-1 10. US-09-956-335-1 10. US-09-956-335-1 10. US-09-956-335-1 10. US-09-956-335-1 10. US-09-956-335-1 10. US-10. 877-146-6 10. US-10. 877-146-6 10. US-10. 877-146-6 10. US-10. 877-146-6 10. US-10. 878-8 10. US-10. 878-8	US-10-240-589C-144 US-10-240-589C-144 US-10-483-289A-5 US-09-932-581-24 US-10-863-075-24 US-10-140-763A-12 US-10-318-294-25 US-10-318-294-25 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17 US-10-081-969-17	RESULT 1  US-10-081-959-93  Sequence 93, Application US/10081969  Publication No. US20030104625A1  Publication No. US20030104625A1  GENERAL INFORMATION:  APPLICANT: Cherg, Lori APPLICANT: Connelly, Sheila APPLICANT: Connelly, Sheila APPLICANT: Forty-Schaudies, Suzanne APPLICANT: Gorziglia, Mario APPLICANT: Gorziglia, Mario APPLICANT: Hallenbeck, Paul APPLICANT: Hallenbeck, Paul APPLICANT: Gorziglia, Mario APPLICANT: Gorziglia, Mario APPLICANT: Gorziglia, Mario APPLICANT: Gorziglia, Mario APPLICANT: Stake, Michael APPLICANT: Steward, John APPLICANT: Steward, David APPLICANT: Steward,
99.6 11276 199.6 26414 199.6 26414 199.9 6 26414 199.9 8 3178 199.8 86.1 4335 199.8 86.1 4335 199.8 86.1 4335 199.8 86.1 4335 199.8 86.1 4335 199.9 86.1 4335 199.9 86.1 4435 199.9 86.1 4430 199.9 86.1 314 99.7 44.9 361 188.7 44.9 44.9 44.9 44.9 44.9 44.9 44.9 44	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	lication US/100  S200310462541  Town:  J. Cheng  A. Lori  Telly, Sheila  Town  To
2 C C C C C C C C C C C C C C C C C C C	273.3 260.4 260.4 256.4 256.4 256.4 256.4 256.4 264.4 199.8	BESULT 1  15-10-081-969-93  SEQUENCE 33, App  SEQUENCE 33, App  APPLICANT: Clen  APPLICANT: Chen  APPLICANT: CON  APPLICANT: CON  APPLICANT: FOR  APPLICANT: STE  APPLICANT: S
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 397; DB 18;
; Pred. No. 8.5e-83;
0; Mismatches 0;
                                                   LOCATION: (3916)..(3970)
OTHER INFORMATION: 5' untranslated region of mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (4029) ... (4050)
OTHER INFORMATION: GW2 primer binding site;
FEATURE:
NAME/KEY: Intron
LOCATION: (4190) .. (4293)
OTHER INFORMATION: Intron 1
US-10-456-830-1
                                                                                                                              FEATURE:
NAME/KEY: protein bind
LOCATION: (3937). (3942)
OTHER INFORMATION: Downstream E-box
FEATURE:
NAME/KEY: CDS
LOCATION: (3971)..(4189)
OTHER INFORMATION: EXON 1
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, APPLICANT: CECh, Thomas R., Lingner, Joachim Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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Best Local Similarity 100.
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-325-810-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (3545)...(3609)
OTHER INFORMATION: Region identical to HBV integration site in huH-4 cell line
FEATURE:
NAME/KEY: protein bind
LOCATION: (3729)...(3734)
OTHER INFORMATION: Upstream E-box
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                            Length 397;
                                                                   FEATURE:
| NAME/KEY: promoter | LOCATION: (1)...(397) | LOCATION: (1)...(397) | CTHER INFORMATION: A 397 bp fragment of the hTERT promoter US-10-081-969-93
                                                                                                                                                                                                                                                                                                                                                                       Indels
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LOCATION: (3916)..(3916)
OTHER INFORMATION: Major transcription initiation site
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                                                                                                                                                                                                                                                                                            100.0%; Score 397; DB 15;
100.0%; Pred. No. 1.7e-82;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 397; Conservative
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ORGANISM: Homo sapiens
TYPE: DNA
ORGANISM: Human
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13208 CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG 13267
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Sequence 1.0.
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Patent No. US20020098582A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gold, Joseph
APPLICANT: Lebkowski, Jane
TITLE OF INVENTION: Tpacked stem cells
FILE REFERENCE: 096/003
CURRENT APPLICATION NUMBER: US/09/783,203
CURRENT APPLICATION NUMBER: 60/253,443
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
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CORGANISM: Homo sapiens
US-09-783-203-1
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US-09-783-203-1
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                                                                                     COUNTRY: USAA
COUNTRY: USAA
COUNTRY: 1911-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/425,810
FILING DATE: 20-Dc-2002
CLASSIFICATION NUMBER: US/09/402,181
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 00-CT-1996
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
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REGISTRATION NUMBER: 42,271
REFERENCE, DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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CTHER INFORMATION: /note= "intron 2"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-325-810-6
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LOCATION: 2702..2804
OTHER INFORMATION: /note= "intron 1"
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SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION: 1..4321
OTHER INFORMATION:
STATE: California
COUNTRY: USA
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                                                                                                                                                       100.0%; Score 397; DB 10;
100.0%; Pred. No. 5.8e-83;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/253,357
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 1
LENGTH: 15418
                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 397; Conservative
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; ORGANISM: Homo sapiens
US-10-141-220-1
                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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US-10-141-220-1
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                                                                                                                     Sequence 1, Application US/09994427A

Perent No. US20020128221A1

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
TILLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT PILING DATE: 2002-02-26
PRIOR FILING DATE: 2000-11-27

FRIOR FILING DATE: 2000-11-27

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 1

SEQ ID NO 1
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                                    13508 GCGCACGTGGAAGCCCTGGCCCCGGCCACCCCGCG 13544
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 397; DB 9;
100.0%; Pred. No. 5.8e-83;
ive 0; Mismatches 0;
                 361 GCGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCCGCG
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| Publication No. US20030032187A1
| GENERAL INFORMATION:
| APPLICANT: Geron Corporation
| APPLICANT: Gold, Joseph D.
| APPLICANT: Schiff, J. Michael
| TITLE OF INVENTION: 096,004 - Seq
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                              LENGTH: 15418
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-995-419A-1
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US-09-994-427A-1
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Length 15418;

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Sequence 1, Application US/10206447
Fublication No. US20030099616A1
Fublication No. US20030099616A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Irving, John
APPLICANT: Schiff, Michael
APPLICANT: Schiff, Michael
TITLE OF INVENTION: DUAL SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE PF
FILE REFERENCE: 085/002
CURRENT APPLICATION NUMBER: 08/10/206,447
CURRENT FILING DATE: 2002-07-25
FRIOR PILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 2
SOFWARE: Patentin version 3.1
                            13389 TCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCCCTT 13447
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100.0%; Pred. No. 5.8e-83;
tive 0; Mismatches 0;
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Matches 397; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-206-447-1
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| Publication No. US2003009598A1
| GENERAL INFORMATION:
| APPLICANT: Geron Corporation
| APPLICANT: Leving, John
| APPLICANT: Leving, John
| APPLICANT: Leving, John
| TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
| TILE REFERENCE: 084,002
| CURRENT FILING DATE: 2001-12-17
| PRIOR PILING DATE: 2001-12-17
| PRIOR FILING DATE: 2000-12-18
| WUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
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LENGTH: 15418
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Query Match
Best Local Similarity
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APPLICANT: Geron Corporation
APPLICANT: McWhir, Jim
APPLICANT: McWhir, Jim
APPLICANT: Golf, Joseph D.
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
FILE REFERENCE: 096,065D-Sequisor, 10510/811,012
CURRENT APPLICATION NUMBER: 0510/995,419
PRIOR APPLICATION NUMBER: 60/253,357
PRIOR APPLICATION NUMBER: 60/253,357
PRIOR APPLICATION NUMBER: 60/253,443
PRIOR APPLICATION NUMBER: 60/253,443
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Lichtsteiner, Serge
APPLICANT: Vasescrot, Alain
APPLICANT: Vasescrot, Alain
APPLICANT: Adams, Robert R.
APPLICANT: Adams, Robert R.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
TITLE OF INVENTION: Telomerase Reverse Transcriptional
TITLE OF INVENTION: Requiatory Sequences and Methods of Using
FILE REFERENCE: 019/246P
CURRENT APPLICATION NUMBER: US/10/674,836
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/244,438
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
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ORGANISM: Homo sapiens
FRATURE:
CTHER INFORMATION: Human TERT promoter
US-10-674-836-1
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Publication No. US20040152189A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  LENGTH: 15418
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US-10-811-012-1
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; Pred. No. 5.8e-83;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 20
SEQ ID NO: 1
SEQ ID NO 1
LENGTH: 15418
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Best Local Similarity 100.0%;
Matches 397; Conservative 0;
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ORGANISM: Homo sapiens
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US-10-811-012-1
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0; Db 10997 GATTCGCGGCCACAGACGCCCAGGACCGCGCTCCCCACGTGGCGGAGGGACTGGGGACCC	60  Qy 181 GGGCACCCGTCCTCCACCTTCCAGCTCCGCGCGGGGACCCCGCGCGGAACCCGGCGCGGAACCCCGCGCGGAACCCCGCGCGGAACCCCGCGCGCGGAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	20   241 TCCCGACCCTCCCGGGCCCACCCCTCCCGGCCCTCCCGGCCCTCCCCTTT	30   301 CCTTTCGGGGCCCCGCCTCTCGGGGGGGGGTTTCAGGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	240 Qy 361 GGGGAGGGGGGGGCCCGGGCACCCCGGG 397 [	300 5026	360	; APPLICANT: Hagen, Gustav ; APPLICANT: Wick, Maread ; APPLICANT: Zubov, Dmitry ; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Hu	FILE REFERENCE: LeA 32 805C1  CURRENT APPLICATION NUMBER: US/10/840,455  CURRENT FILING DATE: 2004-05-06  PRIOR PLING DATE: 1998-12-22  PRIOR APPLICATION NUMBER: US/82,246  PRIOR APPLICATION NUMBER: US 09/582,246  PRIOR PILING DATE: 2000-09-21  PRIOR FILING DATE: 1997-12-24  PRIOR FILING DATE: 1997-12-24	Catalytic peutic Use		CCTTGCTGGCTGCCTGCACCGGGGGGGGGGGGGGGGGGG	Qy         61         CCAGACCCCGGGTCCGCCGGAGCAGCTGCGCTGTGGGGGCCAGGCCGGGCTCCCAGTG	Oy 121 GATTCGCGGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACCCC	60 Oy 181	11957 GGCACCGTCCTGCCCTTCACCTTCCACTCCTCCGCGCGCG	10936 Db 11057 120 Qy 241 10996 Db 11117	
	Oy         1 CCCTCGCTGGCGTCCCTGCACCCTGGAGCGCGCGCGCGCG	Qy         61 CCAGACCCCCGGGTCCGCCGGAGCAGCTGCGCTGTCGGGGCCCAGGCCCGGGCTCCCAGTG           Db         4787 CCAGACCCCCGGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG	Oy         121 GATTCGCGGGCACAGACGCCCTACCCACGTGGCGAGGGACTGGGGACCC           Db         1847 GATTCGCGGCACAGACGCCCAGGACCGCGTCCCCCACGTGGCGAGGACTGGGGACCC	Qy         181 GGGCACCCGGTCCTGCCTTCCACTTCCACTCCGCCTCCTCCGCGCGGGACCCCGCCCCG	Qy         241         TCCCGACCCTCCCGGGTCCCCGGCCCAGCCCCTCGGGGCCCTCCCAGCCCCTCCCGGGCCCCTCCCGGGCCCTCCCGGGCCCTCCCGGGCCCTCCCGGGCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGGCCCCTCCCGGCCCCCC	Oy 301 CCTTTCGGGGCCCGCCCTCTCGTGGGGGGGGGGGAGTTTCAGGCAGG	Oy 361 GGGCACGTGGGAAGCCCTGGCCCCGGCCCCCCCCCCCCC	RESULT 13  US-10-840-455-3  Sequence 3, Application US/10840455  Publication No. US20050032034A1  GENERAL INFORMATION:  APPLICANT: Bayer Aktiengesellschaft  APPLICANT: Hagen, Guetav  APPLICANT: Wick, Maresa	the Gene for the Human ir Diagnostic and Thera	PRIOR APPLICATION NUMBER: PCT/EP98/08216 PRIOR FILING DATE: 1998-12-22 PRIOR APPLICATION NUMBER: US 09/582,246 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21	PRIOR FILING DATE: 1997-12-24 NUMBER OF SEQ ID NOS: 44 SOFTWARE: Patentin version 3.2 SEQ ID NO 3	; LENGTH: 11276 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-840-455-3	Query Match 99.6%; Score 395.4; DB 19; Length 11276; Best Local Similarity 99.7%; Pred. No. 1.5e-82; Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps	Qy         1 CCCTCGCTGGCGTCCCTGGGAGCGGAGCGGGGGGGGGGG		61 CCAGACCCCGGGTCCGCCCGGAGCACTGCGCTGCGGGGCCAGGCCGGGCTCCCAGTG	

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11177 CCTTTCCGCGGCCCCCCCCTCCCCGCGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCT 11236
                                                                                                                      RESULT 15
US-09-733-294A-30
is Sequence 30, Application US/09733294A
j Sequence 30, Application US/09733294A
j Patent No. US2002004558A1
j GENERAL INFORMATION:
j APPLICANT: Breat P. Monia
j APPLICANT: Susan M. Freier
j APPLICANT: Edward V. Wancewicz
j TTLE OF INVENTION: ANTIENES MODULATION OF TERT EXPRESSION
j TTLE OF INVENTION: ANTIENES MODULATION OF TERT EXPRESSION
j TTLE OF INVENTION: 2000-05-07
j PRIOR APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-05-16
j RIOR APPLICATION NUMBER: 09/572,423
j FRIOR FILING DATE: 2000-05-16
j SEQ ID NO 30
j LENGTH: 51552
                                                                            11237 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 11273
                                                   361 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
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NAME/KEY: intron
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NAME/KEY: exon
LOCATION: (21567) ...(21762)
OTHER INFORMATION: exon 3
NAME/KEY: intron
LOCATION: (21763) ...(23851)
OTHER INFORMATION: intron 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEX: exon
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LOCATION: (25550) ...(30196)
OTHER INFORMATION: intron 6
OTHER INFORMATION: exon 6
NAME/KEY: intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAMEX KEY: exon
LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAMEX KEY: 110 TO 1
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION: (23852)...(24032)
OTHER INFORMATION: exon 4
NAME/KEY: Intron
LOCATION: (24033)...(24719)
OTHER INFORMATION: intron 4
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OTHER INFORMATION: exon 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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121 GATTCGCGGGCACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGGACTGGGGACCC 180
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99.6%; Score 395.4; DB 9; Length 51552;
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NAME/KEY: exon
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NAME/KEY: intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (47174)...(47709)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
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Search completed: April 9, 2005, 10:41:30 Job time: 510.69 secs
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9, 2005, 05:45:13 ; Search time 126.15 Seconds (without alignments) 5149.459 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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397
                                                                                                                  April
                                                                                                                                                                                             Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued Patents NA:\*

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3. /cgn2\_6/ptodatca/1/ina/backfiles1.seq:\*

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4	397	100.0	15418	4	US-09-244-438-1	٦,
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14	298.2	75.1	314	4	US-09-916-510A-8	œ
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PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-0CT-1996

APPLICATION NUMBER: US 08/84,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/86,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

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APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

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FILING DATE: 11-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 10-OCT-1997

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PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 7
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SEQ ID NO 1
LENGTH: 15418
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Best Local Similarity 100.
Matches 397; Conservative
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CORGANISM: Homo sapiens
US-09-783-203-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCCTCCGCGCGGGACCCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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Matches 397; Conservative 0; Mismatches 0; Indels 0
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
REFERENCE/DOCKET NUMBER: 015389-002620US
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
TYPE: nucleic acid
STREE: nucleic acid
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LOCATION: 2702..2804
OTHER INFORMATION: /note= "intron 1"
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Patent No. 6576464
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geld, Joseph
APPLICANT: Lebkowski, Jane
TITLE OF INVENTION: Tpacked stem cells
FILE REFERENCE: 096/003
CURRENT APPLICATION UMBER: US/09/783,203
CURRENT FILING DATE: 2001-02-13
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: -
LOCATION: 1..4321
OTHER INFORMATION:
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US-09-783-203-1
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Sequence 1, Application US/09994427A

SERVERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geron Corporation
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: 08709/994,427A
CURRENT FILING DATE: 2002-126
PRIOR APPLICATION NUMBER: 60/253,395
FRIOR RILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEC ID NOS: 17
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Best Local Similarity 100.0%; Score 397; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.2e-71;
Matches 397; Conservative 0; Mismatches 0; Indels 0;
; Score 397; DB 4; Length 15418; ; Pred. No. 3.2e-71; 0; Mismatches 0; Indels 0;
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Sequence 12197, Application US/09949016
; Sequence 12197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: 2000-04-14
; FILE REFERENCE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2070012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
13388 TCCCGACCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTTCCCTT 13447
                                                  13448 CCTTTCCGCGGCCCCCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCTGCT 13507
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Pred. No. 6.8e-71;
0; Mismatches 1; Indels 0;
                                                                                                                             13508 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCG 13544
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| COATION: (1)...(44952)
| OTHER INFORMATION: n = A,T,C or
US-09-949-016-12197
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Best Local Similarity 99.7%;
Matches 396; Conservative
                                                                                                                                                                                                  RESULT 5
US-09-949-016-12197
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                                                                                       GATTCGCGGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGGACCC 180
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GENERAL INCORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Masserot, Alain
APPLICANT: Vasserot, Alain
APPLICANT: Vasserot, Alain
APPLICANT: Geron Corporation
TITLE OF INVENTION: Regulatory Sequences and Methods of Using
TITLE OF INVENTION: Regulatory Sequences and Methods of Using
CURRENT APPLICANTON NUMBER: US/09/244,438
CURRENT FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 15418
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CRGANISM: Homo sapiens
FEATURE:
CTHER INFORMATION: Human TERT promoter
US-09-244-438-1
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Best Local Similarity 100.
Matches 397; Conservative
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LOCATION: (36014)...(37884)
OTHER INFORMATION: intron 10
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 6

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99.6%; Score 395.4; DB 4; Length 44960;
Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30. Application US/09733294A
Patent No. 6492171
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
APPLICANT: Sugan M. Freier
APPLICANT: Edward V. Wancewicz
APPLICANT: Stan M. Freier
APPLICANT: Stan M. Freier
APPLICANT: Stan M. Freier
APPLICANT: Stan M. Freier
APPLICANT: Edward V. Wancewicz
APPLICANT: INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0527
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| LOCATION: (1)...(4456)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-733-294A-30
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CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
NUMBER OF SQ ID NOS: 108
SEQ ID NO 30
LENGTH: 51552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: (24720) ...(24899)
OTHER INFORMATION: exon 5
NAME/KEY: intron
LOCATION: (24900) ...(25393)
OTHER INFORMATION: intron 5
NAME/KEY: exon
LOCATION: (25394) ...(25549)
OTHER INFORMATION: exon 6
NAME/KEY: intron
LOCATION: (25550) ...(30196)
OTHER INFORMATION: intron 6
NAME/KEY: exon
LOCATION: (3550) ...(30292)
OTHER INFORMATION: exon 7
NAME/KEY: intron
LOCATION: (30195) ...(30292)
OTHER INFORMATION: exon 7
NAME/KEY: intron
LOCATION: (30293) ...(30292)
OTHER INFORMATION: intron 6
OTHER INFORMATION: intron 6
OTHER INFORMATION: intron 7
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LOCATION: (21763)...(23851)
OTHER INFORMATION: intron 3
NAME/KEY: exon
LOCATION: (23852)...(24032)
OTHER INFORMATION: exon 4
NAME/KEY: intron
LOCATION: (24033)...(24719)
OTHER INFORMATION: intron 4
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OTHER INFORMATION: exon 9
NAME/KEY: intron
OTHER INFORMATION: (135941)
OTHER INFORMATION: intron 9
NAME/KEY: exon
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LOCATION: (31359)...(33843)
OTHER INFORMATION: intron 8
NAME/KEY: unsure
LOCATION: 31450
                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAME/KEY: intron
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1
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LOCATION: (12951)...(21566)
OTHER INFORMATION: intron 2
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LOCATION: (31273)...(31358)
OTHER INFORMATION: exon 8
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OTHER INFORMATION: exon 10
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LOCATION: (21567)...(21762)
OTHER INFORMATION: exon 3
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OTHER INFORMATION: exon 2
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34325 CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG 34266
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APPLICANT: CALLY Mohan

APPLICANT: WIPSAGMANI, Mohan

TITLE OF INVENTION: RECOMBINATA ADENOVIRUS VECTORS THAT ARE

TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS

FILE REFERENCE: 16153-8394

CURRENT APPLICATION NUMBER: US/09/956,335

CURRENT FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 2

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APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: TOTH, Karoly
APPLICANT: TOTH, Konsantin
APPLICANT: TOTH KONSAMI, Wohan
APPLICANT: TOTH KONSAMI, WOHAN
APPLICANT: DORONIN, KONSANTIN TADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION NUMBER: US/09/956,335
CURRENT PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VEr. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%; Score 354.2; DB 4; Length 35871; 99.2%; Pred. No. 1.2e-62; ive 0; Mismatches 3; Indels 0;
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Patent No. 6627190
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Best Local Similarity 99.23
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.2
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-2
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CORGANISM: Adenovirus
US-09-956-335-1
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LENGTH: 35978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
99.6%; Score 395.4; DB 4; Length 51552;
Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11237 GCGCACGTGGAAGCCCTGGCCCCGGCCACCCCGCG 11273
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Sequence 2, Application US/09956335; Patent No. 6621190; GENERAL INFORMATION:
                                                                                                         NAME/KEY: Intron
LOCATION: (38074)...(41874)
OTHER INFORMATION: intron 11
NAME/KEY: excon
LOCATION: (41875)...(42001)
OTHER INFORMATION: excon 12
NAME/KEY: intron
LOCATION: (42002)...(42881)
OTHER INFORMATION: intron 12
NAME/KEY: intron
LOCATION: (42882)...(42943)
OTHER INFORMATION: excon 13
NAME/KEY: intron
LOCATION: (42944)...(46129)
OTHER INFORMATION: intron 13
NAME/KEY: excon
LOCATION: (46130)...(46254)
OTHER INFORMATION: excn 14
NAME/KEY: intron
LOCATION: (46130)...(46254)
OTHER INFORMATION: excn 14
NAME/KEY: intron
LOCATION: (46255)...(47035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
US-09-733-294A-30
                                                                  CATION: (37885)...(38073)
HER INFORMATION: exon 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: intron
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TYPE: nucleic acid
                                                                    US-08-974-549A-6
34312 GGGCACCCGTCCTCCACCTTCCAGCTCCGCCTCCTCCGCGCGGACCCCGCCCCG 34253
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                                                                                                                                                                                                                                                                                                                                                       TCCCAACCCTCCCGGGTCCCCGGCCCACCTCCCGGGCCCTCCCAGCCCTT 300
                                                                                                                                                                    121 GATTCGCGGGCACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGGACTGGGGACCC 180
                                                                                                                                                                                                                                                                 GGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCCTCCGCGCGGACCCCGCCCCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GATTCGCGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 GATTCGCGGGCACAGACGCCCAGGACGCGCTTCCCACGTGGCGGAGGGACTGGGGACCC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCCTCCGCGCGGGACCCCGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCCCTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 TCCCGACCCTCCCGGGTCCCCGGCCCACCCTCCGGGCCTCCCACCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-956-335-3/c

Sequence 3, Application US/09956335

Sequence 3, Application US/09956335

PRECENT NO. 6627190:

GENERAL INFORMATION:

APPLICANT: WOLD, William

APPLICANT: TOTH, Karoly

APPLICANT: TOTH, Karoly

APPLICANT: MORONIN, Mohantin, Mohantin, APPLICANT: MORONIN, MOHANTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS

FILE REPERENCE: 16153-8394

CURRENT APPLICATION NUMBER: US/09/956,335

CURRENT PILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-956-335-3
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Sequence 6, Application US/08974549A
; Batent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, Milliam H.
; APPLICANT: Andrews, William H.
; APPLICANT: Andrews, Milliam H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BREACHIN Release #1.0, Version #1.30
SUSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-AFR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
ATCORDEY/AGENT INPORMATION:
APPLICATION NUMBER: US 01-OCT-1997
ANDMER: PANAGOLD P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQUENCE CHARACTERISTICS: (115) 576-0300
INFORMATION FOR SEQ ID NO: (116) 576-0300
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US-09-721-456-6
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 CCAGACCCCGGGGTCCGCCCGGAGCAGCTGCGCGTGTCGGGCCCAGGCCGGGGTCCCAGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 CTTCC-TTTCCGCGCCCCCCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCC 356
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Pred. No. 3.7e-60;
0; Mismatches 7; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
                                                                       NAME/KEY: -
LOCATION: 1..4335
OTHER INFORMATION: /note= "genomic DNA insert of pgRN144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2455 TGCTGCGCACGTGGGAAGCCCTGGCCCCGGGCCACCCCCGGG 2495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 TGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 397
                                                                                                                                              NAME/KEY: intron
LOCATION: 2715..2818
OTHER INFORMATION: /note= "intron 1"
                                                                                                                                                                                                                       NAME/KEY: intron
LOCATION: 4173..4326
US-08-974-549A-6
US-08-974-549A-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cech, Thomas R
                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.3%;
Matches 390; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
   single
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-721-456-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "genomic DNA insert of pGRN144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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Pred. No. 3.7e-60;
0; Mismatches 7; Indels 4;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 2-No. 6617110-2000
CLASSIFICATION: cUnknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 01-00T-1996
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-00T-1996
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-00T-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,813
APPLICATION NUMBER: US 08/851,813
APPLICATION NUMBER: US 08/91,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 2715..2818
OTHER INFORMATION: /note= "intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 4173..4326
OTHER INFORMATION: /note= "intron
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4335 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..4335
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GCGGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGAACCCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ACCCCTCCCGGGTCCCCGGGCCCCTCCGGGCCCTCCCAGCCCTTCC-TT
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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                                                                                                                                                                                                                                                                                                                                                            Length 4200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.1%; Score 298.2; DB 4; Length 314; Best Local Similarity 98.7%; Pred. No. 2e-51; Matches 311; Conservative 0; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.2%; Pred. No. 1.5e-59;
Matches 379; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2279 CACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGG 2312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 CACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IGGO, RICHARD D.
APPLICANT: IGGO, RICHARD D.
APPLICANT: BRUNGATION:
ANTI-NEOPLASTIC VIRAL AGENTS
FILE REFERENCE: 604-596
CURRENT APPLICATION NUMBER: US/09/916,510A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: GB 9906815.7
PRIOR FILING DATE: 1999-03-24
015389-002600US
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US-09-916-510A-8
; Sequence 8, Application US/09916510A
; Patent No. 6544507
                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 314
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2215 GATTCGCGGGCAACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACC 2274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Linguer, Joachim

APPLICANT: Linguer, Joachim

APPLICANT: Andemura, Toru

APPLICANT: Morin, Gregg B.

APPLICANT: Morin, Gregg B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPBUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:
                                                                                                                                                               239 CGTCCCG-ACCCCTCCCGGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCC
                                                      2455 TGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCG 2495
                                                                                                                                                                                                                                                                                                                                                                                   357 TGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 397
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FLING DATE: US/08/912,951
FLING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION: A35
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: A35
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
FRIOR APPLICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08912951
Patent No. 6475789
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-912-951-6
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61 GGACCGCGCTCCCCACGTGGCGGAGGGACTCGGGGACCCGGGCACCCGTCCTTCA 120
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1 AGCAGCTGCGCTGTCGGGCCCAGGCCGGGCTCCCAGTGGATTCGCGGGCACAGACGCCCA 60
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APPLICANT: Lichtsteiner, Serge
APPLICANT: Lichtsteiner, Serge
APPLICANT: Vasserot, Alain
APPLICANT: Vasserot, Alain
APPLICANT: Adams, Obert R.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
TITLE OF INVENTION: Telomerase Reverse Transcriptional
TITLE OF INVENTION: Telomerase Reverse Transcriptional
TITLE OF INVENTION: Telomerase Reverse Transcriptional
TITLE OF INVENTION: 1994-02-04
CURRENT APPLICATION NUMBER: US/09/244,438
CURRENT FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 298
TANNA TELOMERA SECOND NOS: 20
TELOM
                                                                                                                                                                                                                                              121 CCTTCCAGCTCCGCCTCCTCCGCGCGCGCACCCCGCCCCGTCCCGACCCCTCCCGGGTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human TERT promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09244438; Patent No. 6777203; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 cceeccaccccccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGCCACCCCGCG 397
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Matches 295; Conservative
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Search completed: April 9, 2005, 07:05:39 Job time : 130.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

9, 2005, 04:29:03; Search time 416.17 Seconds (without alignments) 5647.064 Million cell updates/sec April Run on:

US-10-081-969-93

1 ccctcgctggcgtccctgca.....tggccccggccaccccgcg 397 Perfect score:

Scoring table: Sequence:

4390206 segs, 2959870667 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

8780412 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

N\_Geneseq\_16Dec04:\*

Database

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn1990s:\* geneseqn1980s:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:\*

Aah41091 Telomeras Aa63785 Nucleotid Aa18601 Human TER Ab85497 Lambda cl AGC21253 Lambda cl AGC31253 Lambda cl AdC31242 Human tel Aax88272 Human cat Aas96607 DNA encod ACG41272 CEA gene AGC41272 CEA gene Adn00285 Tumour-sp Aaa94134 Telomeras Ab192335 Chemicall DNA encod CEA gene Recombina Recombina Adr73423 Human tel Adr73427 Human m-h Human tel Human tel Abs98658 Human TER Description Aad27973 | Aav16979 | SUMMARIES ADN00285 AAA94134 ABL92335 ADC21253 ADI33422 AAH41091 AAA63785 AAL38601 ABSS4997 AAL38595 AAX88272 AAS96607 ACC47272 AAD27972 AAD27971 AAD27973 AAV16979 Length DB 15418 15418 15418 15418 35871 35978 51552 1677 Query 100.0 100.0 100.0 82.8 75.1 69.0 100.0 328.6 298.2 273.8 Score 397 395.4 395.4 395.4 376.4 354.2 354.2 Result 000

Aal55438 Specific	Adi80429 Anti-tumo	Aal55435 Specific	Abq76069 Anticance	Abk12706 Human tel	Abv75307 Telomeras	Abv75306 TERT mini	Abz23897 TERT mini	Abk12707 Minimal t	Abs98659 Human TER	Abs98580 Ar17pAE2f	Abz23898 Telomeras	Aad22344 Chemicall		Abl92334 Chemicall	Abz79850 TERT mini	Aad22343 Chemicall	Abv73905 Telomeras	Abv74896 Minimal t	Abz79851 Human sit	Abz22591 Human TER	Adc87060 Human GPC	Acn54594 Cotton an	Adc86738 Human GPC	Acn54596 Cotton an
AAL55438	ADI 80429	AAL55435	ABQ76069	ABK12706	ABV75307	ABV75306	ABZ23897	ABK12707	ABS98659	ABS98580	ABZ23898	AAD22344	ABS98583	ABL92334	ABZ79850	AAD22343	ABV73905	ABV74896	ABZ79851	AB222591	ADC87060	ACN54594	ADC86738	ACN54596
9	12	9	9	9	۵	8	10	9	9	9	10	9	9	9	00	9	9	9	80	10	10	13	70	13
327	327	293	293	261	295	295	295	5928	245	955	240	1404	403	4356	144	1404	89	78	78	78	3163	629	3133	588
65.6	65.6	65.2	65.2	64.6	64.6	64.6	64.6	64.6	61.5	61.5	54.5	53.5	50.3	45.6	36.3	33.7	22.2	19.4	19.4	19.4	17.8	17.3	17.2	17.1
260.4	260.4	259	259	256.4	256.4	256.4	256.4	256.4	244	244	216.4	212.2	199.8	181.2	144	133.6	88	77	77	77	9.07	9.89	68.2	67.8
21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

ABS98658 standard; DNA; 397 ABS98658; RESULT 1 ABS98658 

ВР

Human TERT promoter sequence #1. (first entry) 17-DEC-2002

Virus; viral vector; adenoviral nucleic acid backbone; breast cancer; inverted terminal repeat; ITR; termination signal sequence; lung cancer; ESF responsive promoter; adenoviral packaging signal; prostate cancer; neoplastic condition; colon cancer; cytostatic; immunostimulant; gene therapy; human; TERT; promoter; ds.

W0200267861-A2 Homo sapiens

06-SEP-2002

22-FEB-2002; 2002WO-US005300

23-FEB-2001; 2001US-0270922P. 01-JUN-2001; 2001US-0295037P. 14-JAN-2002; 2002US-0348670P.

(NOVS ) NOVARTIS PHARMA AG

S; , Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly , Clarke L, Phipps S, Cheng C; Ennist DL, Jakubczak JI Police SR,

WPI; 2002-706950/76.

Recombinant viral vector comprising an adenoviral nucleic acid backbone, useful for treating neoplastic disorders such as lung, breast, prostate or colon cancer.

Claim 11; Page 21; 226pp; English.

The present invention relates to a new recombinant viral vector

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X S X & & X E X E X B X X X X B
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comprising an adenoviral nucleic acid backbone, where the backbone comprises in sequential order, a left inverted terminal repeat (ITR), a termination signal sequence, an SEF responsive promoter which is operably linked to a gene essential for replication of the recombinant viral vector, an adenoviral packaging signal and a right ITR. The methods and compositions of the present invention are useful for treating a neoplastic condition such as lung, breast, prostets or colon cancer. The viral vectors are useful in studying methods of killing neoplastic cells in vitro or in animal models. The present nucleic acid sequence represents a human TERT promoter of the invention
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100.0%; Score 397; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 397; Conservative 0; Mismatches 0;
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(KIMJ/) KIM J.
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The invention relates to a transcriptional regulatory sequence with a human telomere reverse transcriptase (hTERT) promoter linked to a nucleotide sequence comprising one or more c-byc binding sites and/or one or more Spl binding sites and/or one composition are useful for treating cancer, e.g. stomach, lung, ovarian, liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer. This sequence corresponds to the wild type human telomerase reverse transcriptase (hTERT) promoter sequence used to generate the novel sequence of the
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                                                                                                                                              New transcriptional regulatory sequence with a human telomere reverse transcriptase promoter, useful for treating cancer, e.g. stomach, lung, ovarian, liver, panoreatic, bladder, colon, cervical, breast, brain, or head and neck cancer.
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The invention relates to a transcriptional regulatory sequence with a human telomere reverse transcriptese (hTRRT) promoter linked to a nucleotide sequence comprising one or more c-Myc binding sites and/or one or more Spl binding sites. The transcriptional regulatory sequence and composition are useful for treating cancer, e.g. stomach, lung, ovarian, liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder, colon, cervical, breast, brain, or had and neck cancer. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transcriptional regulatory sequence with a human telomere reverse transcriptase promoter, useful for treating cancer, e.g. stomach, lung, ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer.
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bound moiety= "Spl transcription factor"
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bound moiety= "Spl transcription factor"
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'bound moiety= "Sp1 transcription factor"
775. .780
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/bound_molety= "c-Myc protein"
228. .236
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bound_moiety= "c-Myc protein"
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corresponds to the modified human telomerase reverse transcriptase (hTERI) promoter sequence containing the extra c-Myc and Spl binding site sequences.
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                                                                 Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;
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Lebkowski JS;

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             This invention relates to a method for isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants. The method is useful in gene localisation and classification analysis, studying gene development networks and function networks, and designing drugs based on regulatory sequences of the phenotypes for disease treatment. The present sequence represents DNA encoding a telomere reverse transcriptase (TERT), which is used in an example illustrating the use of the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the human TERT promoter and gene from pGRN142
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                                                                                                                                                                           100.0%; Score 397; DB 4; Length 3962; 100.0%; Pred. No. 2e-56; cive 0; Mismatches 0; Indels 0
                                                                                                                                               Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;
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Matches 397; Conservative 0; Mismatches
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Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardoza LM;

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                                                                                                       New polynucleotides comprising cis-acting transcriptional control sequences, e.g. promoter sequence, of telomerase reverse transcriptase genes, useful in the treatment of cancer.
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                                                                                                                                                                                                                 Claim 9; Page 58-61; 63pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a polynucleotide comprising an encoding sequence for a glycosyltransferase, under control of a heterologous tumour specific or tissue specific transcriptional control element, where expression of the polynucleotide in a human cell causes the cell to express a cell-surface carbohydrate determinant to which some or all mumans have a naturally occurring antibody. The polynucleotide of the invention is useful for killing cancer cells and for preparing a medicament for the treatment of cancer. The polynucleotide sequence of the invention can be used to treat disorders by gene therapy. This polynucleotide sequence represents the human TRRT (telomerase reverse transcriptase) promoter and upstream sequence related to the invention
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                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding glycosyltransferase enzymes including histo blood group transferase useful for treating conditions associated with hyperproliferation, such as cancers and other neoplasias.
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tissue specific; transcriptional control element; cancer cell; gene therapy; human TERT; telomerase reverse transcriptase; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 397; DB 6;
100.0%; Pred. No. 1.6e-56;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 17-20; 49pp; English.
                                                                                                                                                     26-NOV-2001; 2001WO-US044306.
                                                                                                                                                                                       27-NOV-2000; 2000US-0253395P
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Matches 397; Conservative
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                                                                                                                                                                                                                        (GERO-) GERON CORP
                                                                                     WO200242468-A2
                                                     Homo sapiens.
                                                                                                                     30-MAY-2002
                                                                                                                                                                                                                                                          Schiff MJ;
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The present invention relates to a new replication-conditional virus with a genome comprising adenovirus replication genes and one or more adenovirus feterologous gene (s) that functionally replaces one or more adenovirus gene (s) required for replication or assembly of the virus. The invention is useful for killing a cancer cell (such as lung, pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma), killing a call expressing TERT (telomerase reverse transcriptase), and in preparing a medicament for treating cancer and a condition associated with increased expression of TERT in affected cells, in a subject. The invention is also useful for producing replication defective adenovirus vector which is useful for transfent expression of a second defective adenovirus vector which is useful for transfent expression of a second defective adenovirus vector which is useful for transfent expression of a second defective adenovirus vector which is useful for transfent expression of a second defective and on the condition are processed and the condition of a second defective and condition are processed and condition of a second defective and condition are processed and condition as a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterologous therapeutic gene to correct a congenital defect, introducing proinflammatory or antiinflammatory activity, enhancing telomerase function, and delivering heterologous effector genes that induce killing of the transduced cells. The invention is more safe for use in cancer therapy. The present nucleic acid sequence represents the human TERT sequence contained within a lambda clone sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel replication-conditional virus useful for cytolysis of target cells e.g. cancer cells and preparing a medicament for treating cancer, comprises heterologous replication element in an adenovirus-based
                                                                                                                                                              Telomerase reverse transcriptase; TERT; replication-conditional virus; adenovirus replication gene; cancer cell; lung; pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma; cytolysis; replication defective adenovirus vector; congenital defect; proinflammatory; antinflammatory; heterologous effector gene; cancer therapy; cytostatic; gene therapy; lambda clone; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "Human telomerase reverse transcriptase (hTBRT)
sequence including the hTBRT promoter and upstream
                                                                                                                          Lambda clone containing human TERT genomic insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "From Lambda clone"
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                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
ABS54997 standard; DNA; 15418 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence"
15376. .15418
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                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda.
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Synthetic.
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ADC21253 standard; DNA; 15418
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                                                                                                                                                                                                             CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCCAGTG 120
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                                                                                    Gaps
Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
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                                           Length 15418;
                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA of plasmid pGRN144 containing human hTERT gene.
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                                      100.0%; Score 397; DB 6; 100.0%; Pred. No. 1.6e-56;
                                                                                  0; Mismatches
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27-NOV-2000; 2000US-0253443P
13-FEB-2001; 2001US-00783203
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                                                          Best Local Similarity 100.
Matches 397; Conservative
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Unidentified
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The invention relates to a system for depleting a cell population of undifferentiated stem cells, by introducing nucleic acids of structure P-X, where X is a nucleic acid encoding product that is lethal to a cell in which it is expressed; or renders a cell in which it is expressed to which it is expressed; or renders a cell in which it is expressed to an external agent, and P is a usceptible to the lethal effect of an external agent, and P is a transcriptional control element causing X to be preferentially expressed in the undifferentiated stem cells. The system is used for depleting a cell population (preferably, human embryonic stem cells) of undifferentiated stem cells. A population of differentiated cells is useful in regenerative medicine, and for preparing antibodies and cDNA libraries that are specific for a differentiated phenotype. The cell populations are also useful for drug screening and therapeutic applications. The differentiated cells are useful for tissue constitution or regeneration in a human patient in need of treatment. The cells are administered in a manner that permits to graft to the intended tissue side and reconstitute or regenerate the functionally deficient area. The neural progenitor cells are useful for treatment in the constitution or regenerate the sequence of the constitution or regenerat
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Depleting a cell e.g., human embryonic stem cell population of undifferentiated stem cells (UC) for use in regenerative medicine comprises genetically altering UC in a population to express nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia, Huntington's disease, Parkinson's disease, multiple sclerosis, leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte precursors are useful for assessing animal models for ability to repair liver damage. The cardiomyocyte population is useful for assessing animal models for cryonipury, regenerating cardiac muscle and to treat insufficient cardiac function. This polynucleotide sequence represents the DNA of plasmid pGRN144 containing the human hTERT gene relating to
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100.0%; Pred. No. 1.6e-56;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Example 9; Page 62-66; 67pp; English.
                                                                                                                                                                                   encoding a lethal product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 397; Conservative
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13208 cchakcccccaatecaccakakakakakakatarakaaccakaccaadarakata 13267

GATTCGCGGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGAGGGACTGGGGACCC GATTCGCGGGCACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGGACTGGGGAACCC 181 GGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCCTCCGCGGGGGGACCCCGCCCCG

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13508 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGG 13544 GCGCACGTGGGAAGCCCTGGCCCCGGGCCACCCCCGCG 397

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CCTTTCCGCGGCCCCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCT

301 13448

360

13388 TCCCGACCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTT

TCCCGACCCCTCCCGGGTCCCCGGCCCCAGCCCCTCCGGGCCCTCCCAGCCCCTTCCCCTT

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13328

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The present invention relates to a viral vector comprising first and second genes controlled by heterologous control elements, where the first gene is a preferentially expressed in cells expressing human telemerase reverse transcriptional control element for a tissue or tumour context than TERT, and where transduction of the vector into a mammalian cell expressing TERT causes the death of the control of a progeny. In particular, the second gene may be under the control of a transcriptional control element for a tissue specific gene selected from albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial creatine kinase, myelin basic protein, glial fibrillary acidic protein, and neuron-specific enolase. The second gene may be under the control of a transcriptional control element for a human telomerase RNA component (hTR). The vector of the invention is useful for killing a cancer cell, or treating a subject for a condition associated with increased expression of TERT in affected cells. The vector is also useful in the preparation of a medicament for treatment of a condition associated with concert, prostate cancer, muscle cancer, neural cancer, lung cancer, pancratic cancer, medulloblatoma, cervical carcinoma, fibrosarcoma, and osteocatic cancer, medulloblatoma, represents a lambda clone concert, and especially invertible cancer, medulloblatoma, represents a lambda clone concert, and cancer and concert, and cancer and concert, and concert, and cancer and concert, and cancer and concert, made cancer and cancer and concert, and cancer and cancer and cancer and concert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New dual specificity vectors driven by the telomerase promoter, useful for killing or slowing the growth of tumor cells, or for treating cancer, e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
                                                                                                                                                                    Viral vector; heterologous control element; gene expression; human telomerase reverse transcriptese; hTERT; tumour specific gene; cell death; transcriptional control element; tumour secriptional control element; human telomerase RNA component; hTR; cancer cell; liver cancer; profetae cancer; meucle cancer; neural cell cancer; lung cancer; panareatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma; panareatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma; setessarcoma; lambda clone; lambdaGphis; human; de.
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                                                                                                                        Lambda clone (lambdaGphi5) containing human TERT DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1, Page 13-20, 25pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2001; 2001US-0308029P
                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Bacteriophage lambda.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCHI/) SCHIFF J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KARPF D B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003099616-A1
                                                                         18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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Schiff JM;

telomerase promoter and at least one viral El gene. Specifically, the El genes are ElA, IRES and ElB and the human telomerase promoter is preferably hrERT. The present invention describes a virue containing this polymucleotide and an anticancer agent that replicates efficiently in tumour cells and causing cell death. As such, it can be used for the treatment of cancer, in particular cancer of the stomach, large intentine, lung, liver, prostate, pancreas, digestive tract, bladder, mammary gland, uterue, thyroid gland and ovary. Accordingly, this composition exhibits cytostatic activity. This polymucleotide sequence is gene This invention relates to a novel polynucleotide comprising a human El; ElA; IRES; ElB; anticancer; Polynucleotide comprising a human telomerase promoter and an El Kawashima T; KANS-) KANSAI TECHNOLOGY LICENSING ORG CO LTD Human telomerase promoter (hTERT) DNA SegID 4. Shirakiya Y, Example 1; SEQ ID NO 4; 34pp; Japanese. human telomerase promoter; human; E' cell death; cancer; cytostatic; ds. Kyo S, ADI33422 standard; DNA; 455 BP 07-JUL-2003; 2003WO-JP008573. 08-JUL-2002; 2002JP-00198941. (first entry) Tanaka N, WPI; 2004-099391/10 FUJIWARA T. TANAKA N. WO2004005511-A1 treating cancer (KYOS/) KYO S Homo sapiens 22-APR-2004 Pujiwara T, 15-JAN-2004. ADI33422; (FUJI/) (TANA/) RESULT 10 ADI33422 

for

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Gaps

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0; Indels

100.0%; Score 397; DB 10; 100.0%; Pred. No. 1.6e-56; iive 0; Mismatches 0;

Matches 397; Conservative

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Local Similarity

Query Match

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containing the product of the invention can be linked with DNA encoding an anti-tumour protein or reporter protein. The constructs are useful for identifying candidate substances that modulate the activity of the telomerase regulatory region. The constructs can be used in cancer
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                                                                                                                                                                                                                                                                                                                                                   CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCGCTGTCTCTCGGGGCCAGGCCGGGCTCCCCAGTG
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                                                                                                                    Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;
                                                                                                                                                                DB 2; Length 5126;
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11274. .47813
/teg= b
/product= "TERT"
/note= "Telomerase reverse transcriptase"
11493. .11596
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                                                                                                                                                                Score 395.4; DB 2;
Pred. No. 3.5e-56;
0; Mismatches 1;
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11597. .12950
/*tag= d
/number= 2
12951. .21566
/*tag= e
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                                                                                                                                                                Query Match
Best Local Similarity
Matches 396; Conserv
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AAS96607
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                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                             CCAGACCCCCGGGTCCCCCCGGAGCAGCTGCCGCTGTCGGGCCCAGGCCCGGGCTCCCAGTG
                                                                                                                                                                                                                                                                          CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG
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                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human catalytic telomerase subunit 5'-flanking regulatory DNA.
              the human telomerase promoter (hTERT) DNA of the invention
                                                                                           DB 12; Length
                                                                                                                                 1, Indels
                                                      Sequence 455 BP; 41 A; 212 C; 142 G; 60 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG 397
                                                                                             Score 395.4; DB 12
Pred. No. 5.2e-56;
                                                                                             Query Match 99.6%; Score 395.4; Best Local Similarity 99.7%; Pred. No. 5.2e Matches 396; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridises with and inhibits the expression of TERT. A series of oligonucleotides were compound to target different regions of the human TERT RNA. These were 20 nucleotides in length and composed of a central gap region consisting of the 12 deoxymucleotides, flanked on both sides (5' and 3' directions) by five-nucleotides. The compounds were composed of 2'-methoxyethyl (2'-MOE) nucleotides. The compound serve analysed for their effect on human CTERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PCR). The compound is useful for inhibiting the expression of TERT in cells or tissues, for treating a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell crowth (preferably, cancer cell growth), in antisense therapy and for diagnostics and therapeutics. This sequence encodes human telomerase reverse transcriptase (TERT) #1, and is used to create antisense coligonucleotides which modify TERT expression, described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 Freier SM, Wancewicz E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 19; Page 112-138; 154pp; English.
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07-DEC-2000; 2000US-00733294
                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                   Gaarde WA,
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P-PSDB; AAU72735.
                                                                                                                                                                                         WO200188198-A1
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CCAGACCCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCCAGGCCGGGCTCCCAGTG

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Score 395.4; DB 6; Length 51552; Pred. No. 2.4e-56; 0; Mismatches 1; Indels 0;

Query Match
Best Local Similarity 99.7%;
Matches 396; Conservative

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GATTCGCGGGCACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGGACTGGGGACCC

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The invention relates to a recombinant adenovirus vector which overexpresses an adenovirus death protein (ADP) and which is replication-restricted to cells expressing telomerase, comprises a human telomerase reverse transcriptase promoter (hTERT) and at least one inactivating mutation in the E3 region. The vector of the invention is useful in vitro for promoting death of a cell expressing telomerase, and for promoting death of a cell expressing telomerase, and for promoting death of neoplastic cells in a patient. The adenovirus vector is an efficiant and effective anticancer agent that could specifically target neoplastic cells, while replicating poorly or not at all in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant adenovirus vector useful for destroying neoplastic cells, comprises a human telomerase reverse transcriptase promoter and at least one inactivation mutation in the B3 region.
                                                                                                                                                                                                                                                                                        241 CCCCGGCCCCACCCCTCCGGGCCCTCCCTTTCCGCGGCCCCGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase; human; telomerase reverse transcriptase promoter; TERT; neoplastic cell; cancer; KD3-TERT; ElA region; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                 CTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTGCTGCTGCGCACGTGGGAAGCCCT 378
CCCGGCCCAGCCCTCCGGGCCCTCCCAGCCCCTTCCTTTCCGCGGCCCCGCC
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                                                                                                               181 freactrice de rececrete de consece de consecue de 
                                                                         CCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGGACCCGGGCACCCGTCCTGCCCC
                                                                                                                                                                      199 TTCACCTTCCAGCTCCGCCTCCTCCGCGGGGACCCCGCCCCGGTCCCGACCCCTCCCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant adenovirus vector KD3-TERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 28-44; 64pp; English.
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AAD27972 standard; DNA; 35871 BP.
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20-SEP-2000; 2000US-0233872P.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                         319
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                                                               11177 CCTTTCCGCGGCCCCCCCTCTCCTCGCGCGCGGGTTTCAGGCAGCGCTGCGTCTTGT36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to expressing gene product in a cell type-
preferential manner. The method involves providing a first expression
cassette having a cell type-preferential promoter, providing a second
expression cassette having an inducible promoter, and transferring the
first and second expression cassettes into a cell in which the cell type
specific preferential promoter is active. The methods and compositions
of the present invention are useful for treating cancers of the brain,
head and neck, esophagus, thyroid stomach, colon, liver, kidney,
prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressing gene products in a cell type-preferential manner with a binary or bicistronic expression system, useful for treating cancers of the brain, head and neck, esophagus, thyroid, stomach, colon, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 CCGGAGCAGCTGCGCGGGCCAGGCCGGGCTCCCAGTGGATTCGCGGGCACAGACG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pression; promoter; cytostatic; gene therapy; antisense therapy; cis-acting; CEA gene; ds.
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Pred. No. 6.7e-53;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 378 BP; 35 A; 178 C; 121 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       11237 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGG 11273
                                                                                                                                                                                                                              361 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 139; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                     ACC47272 standard; DNA; 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Matches 377, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC47272;
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ACC47272
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tissue, and efficiently spreading to neighbouring neoplastic cells, thereby maximising its cancer-killing ability. The presence of human telomerase reverse transcriptase promoter allows restriction of replication of the adenovirus to cells expressing telomerase without the need for complementation to achieve replication competence in these cells. The present sequence is adenovirus vector KD3-TERT which comprises an ADP gene, a hTERT promoter, and a mutation in the B1A region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human, telomerase reverse transcriptase promoter; TERT; neoplastic cell; cancer; GZ3-TERT; B3 region; mutant; ds.
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                                                                                                                                                                                                                                                            CCAGACCCCCGGGTCCCCCCGGAGCAGCTGCGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG
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                                                                                                               Sequence 35871 BP; 8238 A; 10114 C; 10001 G; 7518 T; 0 U; 0 Other;
                                                                                                                                           Score 354.2; DB 6; Length 35871;
Pred. No. 1.3e-49;
0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant adenovirus vector GZ3-TERT
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Best Local Similarity 99.2%;
Matches 356; Conservative (
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coverexpresses an adenovirus death protein (ADP) and which is replication-
coverexpresses an adenovirus death protein (ADP) and which is replication-
crestricted to cells expressing telomerase, comprises a human telomerase
contexpresses promoter (hTRRT) and at least one inactivating
contexpresses promoter (hTRRT) and at least one inactivating
contexpresses region. The vector of the invention is useful in vitro
contexpressing telomerase, and for promoting
contexpressing telomerase, and for promoting
contexpressing telomerase, and for promoting
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contexpresser transcriptase promoter allows restriction of
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colls the present sequence is adenovirus vector GZ3-TRRT which comprises
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Novel recombinant adenovirus vector useful for destroying neoplastic cells, comprises a human telomerase reverse transcriptase promoter and at least one inactivation mutation in the E3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TCCCGACCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCTTCCCCTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.2%; Score 354.2; DB 6; Length 35978; 99.2%; Pred. No. 1.3e-49; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an ADP gene, a hTERT promoter, and a mutation in the E3 region
                                                                                                                                              The invention relates to a recombinant adenovirus vector which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 9, 2005, 06:08:12 Job time : 422.17 secs
                                                                                                 Claim 2; Page 12-28; 64pp; English
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Best Local Similarity 99.2
Matches 356; Conservative
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AG448267 AG435689 AG435591 AL104949 CL478793 CL478793 CB905393 CF876920 BZ051861 BF865678

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AL573255 A CL493953 S CL515456 S AG320910 N AG360980 N

jnr57a10. 963061E04

AL573255

Sequence:

Run on:

Searched:

Database

Result ģ υ

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Lattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Elect Submission

Listed (17-002) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriseger.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSNg01. For BAC library availablity, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9199

e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG334095 1285 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-124N12.TJ, genomic survey
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Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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1. .1285
/ organism="Mus musculus molossinus"
/ organism="Mus musculus molossinus"
/ mol_type="genomic DNA"
/ sub_species="molossinus"
/ db_xref="taxon:57486"
/ clone="MSMg01-124N12.TJ"
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AG435689
AG435591
CNS0153F
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BZ051861
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(c) 1993 - 2005 Compugen Ltd.
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Maximum DB
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/tissue type="mixture of kidney and spleen" /clone\_lib="MSMg01 Mouse Male BAC Library"

Drosophi] Pan trogl

222109876 2321098765432109876

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86 ccercccaccccrcccaeerccccaecccaacccccrccaecccrccaacccrcca
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SM Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,

Warren,W., Gravee,T., Mardis,E. and Wilson,R.

Gallus gallus BAC End Reads

L. Unpublished (2003)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 182000

Seg primer: Sp6 ATTTAGGTGACACTATAG
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                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                    86 CCGTCCCGACCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCC
                                                                                                                                                                                             Gaps
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                                                                         Length 1285;
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                                                                   31.5%; Score 77.2; DB 9;
58.0%; Pred. No. 7e-05;
:ive 0; Mismatches 92;
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/clone_lib="CH261"
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-172NS"
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High quality sequence stop: 136.
Location/Qualifiers
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                                                                                                                                      Matches 127; Conservative
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Contact: Sessions A Applied Trait Genetics Sympatratic Genetics Sympatratic Genetics Sympatratic Genetics Sympatra Biotechnology Inc.
Sympatra Biotechnology Inc.
Email: allen.sessions@syngenta.com
ABRC Stock Number CS845346; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
                    1539
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                                                                                                                            Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 941)
Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D.,
Dietrich, B., Ho, P., Bacaden, J., Ko, C., Clarke, J. D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B.,
Mitzel, T., Kataglir, F., Glazchrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
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/clone="SAIL_1236_D06.v1"
/clone="Ib="SAIL_Collection"
/note="T-DNA_1eft border sequences were isolated using
modified TAIL-PCR strategy"
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146 CTTCCTTTCCGCGGCCCCGCCCTCTCCTCGCGCGCGAGTTTCAGGCAGCGCTGCGTCCT
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/mol_type="genomic DNA"
/ecotype="Columbia"
                                                                                                                                                                                         206 GCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
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On May 15, 2003 this sequence version replaced gi:30774610.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT & vector. Library
was not normalized Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                         BX427015 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODM006XN18 3-PRIME, mRNA sequence.
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305 CCCGGSCCCGCACCCSCTSCCCGCCSCCGWGGMCSCCSCCGSSYCCMCSGCS 246
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_Xref="taxon:9606"
/clone="CSODMO06XN18"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
                                                                                            212 CACGTGGGAAGCCCTGGCCCCCGGCCACCCCGG
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                                                                                                                                                                                                                                                CNS03JN0 566 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 031B04 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terrandon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 969)
S Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katsgiri, F., Glazebrook, J., Law, M., and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system

L Plant Cell 14 (12), 2985-2994 (2002)
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Sympanta Biotechnology Inc.
Sympanta Biotechnology Inc.
Email: allon.sessions68yngenta.com
ABRC Stock Number CS812359; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not class: TDNA tagged.
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CL477043 969 bp DNA linear GSS 01-APR-2004 SALL.267 A03.v1 SAIL Collection Arabidopsis thaliana genomic clone SAIL.267, A03.v1, genomic survey sequence.
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/clone_lbe="SAIL_Collection"
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modified TAIL-PCR strategy"
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Arabidopsis thaliana (thale cress)
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Contact: Sessions A Applied Trait Genetics Symptomeral Sympolical Trait Genetics Symponta Biotechnology Inc.
Symponta Biotechnology Inc.
Email: allen.sessions@syngenta.com
ABRC Stock Number CS61263; T-DNA left border flanking sequences of ABRC Stock Number CS61263; T-DNA left border flanking sequences of Syngenta Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Location/Qualifiers
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BRY 4732 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence.
BQ608819.1 GI:21558158
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eparadeophyta, Germatophyta, Germatophyta, Germatophyta, Core eudicots, rosida, eurosida II, Brassicales, Brassicaces, Arabidopsis.

1 (bases 1 to 988)

2 sessions, A. Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., A high-throughput Arabidopsis reverse genetics system

2 high-throughput Arabidopsis reverse genetics system

2 cell 14 (12), 2985-2994 (2002)
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/organism="Arabidopsis thaliana"
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/clone="Lib="SAIL_Collection"
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56.3%; Pred. No. 0.00024;
Live 0; Mismatches 107; Indels
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Matches 138; Conservative
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241 CCGC 244
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jnr64f12.b1 B.oleracea001 Brassica oleracea genomic, genomic survey
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Contact: Lambrecht M
Contact: Lambrecht M
Carnegia Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rheedacoma stanford.edu.
Email: rheedacoma stanford.edu.
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                             1 (bases 1 to 468)
Clarke, B., Lambrecht, M. and Rhee, S.Y.
Arabidopsis genomic information for interpreting wheat EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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(days post anthesis)
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22478026
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Washington University School of Medicine
Baail: submissions@watson.wustl.edu
Plate: jnr64 row: f column: 12
Seq primer: -21UPpOT forward
Class: shotgun
Pooldeae, Triticeae, Triticum.
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01.
Li Unpublished
Li Chases 1 to 1233)
Lattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Li Submission
Li Chases 1 to 1230)
List Submission
Li Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Li Charlishattoriogsoc. Tiken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81.45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
Library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-288-36-9189, fax: 81-298-36-9199
                                                                                               1...794
| organism="Brassica oleracea"
| organism="Brassica oleracea"
| mol-type="genomic DNA"
| db xref="taxon:312"
| clone_lib="B.oleracea001"
| note="vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High quality sequence start: 137
High quality sequence stop: 551.
Location/Qualifiers
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Mus musculus molossinus
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Gaps

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La vacation, Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submission

Ly birect Submission

Ly Submitted (17-NOV-2003) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-maili hattoriager.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG382572 1270 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-193C09.T7, genomic survey
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                   /ecory.pe=_columning
/db_xref="teatural]102"
/clone="SAIL_1249_G02.v1"
/clone="lb="SAIL_Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
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BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                         Length 949;
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30.0%; Score 73.4; DB 9; Length 9
Best Local Similarity 57.1%; Pred. No. 0.00037;
Matches 125; Conservative 0; Mismatches 94; Indels
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/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
                        thaliana"
                                                 /mol_type="genomic_DNA"
/ecotype="Columbia"
                           organism="Arabidopsis
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Sessions, A., Burke, B., Presting, G., Aux, G., McElver, J., Patton, D., Betrich, B., Ho, P., Bacwaden, J., Ko.C., Clarke, J.D., Cotton, D., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. Mighethroughput Arabidopsis reverse genetics system
Plant (12), 2985-2994 (2002)
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Pred. No. 0.00033;
0; Mismatches 90; Indels 0
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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Best Local Similarity 58.5%;
Matches 127; Conservative (
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1 (hose 1 to 1081)
Sessions, A., Burke, B., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Kazagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system
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Syngenta Biocechnology Inc.

3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA

Email: allen.sessions@syngenta.com

ABRC Stock Number CS644896, T-DNA left border flanking sequences o

Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).

Sequences represent a pool of amplified genomic regions and not

single contiguous sequences.

Class: TDNA tagged.
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                                                                                                                                                                 Length 1270;
                                                                                /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-193C09.T7"
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/db xref="taxon:3702"
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Applied Trait Genetics
                                                             /sex="male"
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou. Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.ip, URL:http://hgp.gsc.riken.go.ip/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpenzee BAC library PTB This BAC end was generated during the RkD process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-136K03.F, genomic survey sequence.
AG126157
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
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BAC end sequences of Library PTB
Unpublished
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                           29.9%; Score 73.2; DB 9; Length 1081; 56.5%; Pred. No. 0.0004; ive 0; Mismatches 104; Indels 0
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No. 0.00049;
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .759
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                Location/Qualifiers
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Pan troglodytes
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Gaps

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97; Indels

0; Mismatches

Matches 122; Conservative

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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/db_xref="taxon:3712"
/dbo=lib="B.oleracea001"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas OBborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                          BZ050815 675 bp DNA linear GSS 09-OCT-2002 jnr64a12.bl B.oleracea001 Brassica oleracea genomic, genomic survey sequence.
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Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 675)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                           CCCCCCCCCTCCCGACCCTCCCGGGTCCCCGGCCCCTCCGGGCCCTCCCAGC 138
                                                                                    CCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCC 145
                                                                                                                                                                    CTTCCTTTCCGCGGCCCCGCCCTCTCCTCGCGGCGCAGTTTCAGGCAGCGCTGCGTCCT 205
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      CCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCTCCGCGCGGGGGACCCCGCC
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                                                                                                                                                                                                                                                 GCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGC 244
                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Washington University School of Medicine
mail: submissions@wateon.wustl.edu
Plate: jnr64 row: a column: 12
Seq primer: -21UPpOr forward
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High quality sequence stop: 535.
Location/Qualifiers
1. 675
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BZ050815
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Search completed: April 9, 2005, 10:27:49 Job time: 2005.54 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB & Maximum DB &

Database

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PAT 10-DEC-2003
AF114847 Homo sapi
AR407124 Sequence
AR403723 Sequence
AR403725 Sequence
E36796 Human telom
AX303087 Sequence
AX810041 Sequence
BD011047 Human tel
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                AR243331 8
AB018788 B

    .397
    /note="A 397 bp fragment of the hTERT promoter"

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Patent: WO 02067861-A 93 06-SEP-2002;
Location/Qualifiers
1. .397
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AR455896
AX817781
AX817781
AC112753
AX280012
AX817785
AX817785
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183506
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Compugen Ltd.
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                      GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    nucleic search, using sw model
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AR390473
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seq length: 200000000
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1504 GGGCACCCGTCCTGCCCCTTCACCTTCCAGCTCCGCCCTCCCCCGCGCGAACCCCGCCCCC 1563
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                               1384 CCAGACCCCGGGTCCGCCCGGAGCAGCTGCGCTGTCGGGGCCAGGCCGGGCTCCCAGTG
                                                                                              1444 GATTCGCGGGCACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGGGACTGGGGACCC
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         CCAGACCCCCGGGTCCGCCCGGAGCTGCCGCTGTCGGGGCCAGGCCCGGGCTCCCAGTG
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Morin,G.B. and Andrews,W.H.
Promoter for telomerase reverse transcriptase
Patent: US 6610839-A 6 26-AUG-2003;
Location/Qualifiers
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Sequence 6 from patent US 6610839.
AR390473
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/codon start=1
/producft="telomerage reverse transcriptase"
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AAFRALVAGCUVCWPWDARPPPAAPSFRQ"
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Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
region and partial cds.
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Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.
Direct Submission
Submitted (15-OCT-1998) Laboratory of Molecular Carcinogenesis,
National Institute of Environmental Health Sciences, 111 T. W.
National List, NC 27709,
USA
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                               TCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCCTCCGGGCCCTCCCAGCCCCTCCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TERT"
1. 1665
/gene="TERT"
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/product="telomerase reverse transcriptase"
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1. .2043
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/chromosome="s"
/map="5p15.33"
1. .>2043
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/gene="TERT"
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LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
PGARRGGSAARSLEPLRYRRRDAAPEDERTPYGOGSWAHDGYRRGBDSDGFCVVSPA
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SGDKEQLRPSFLLSSLRRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYRQMRPL
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LLRQHSSPWQVCGFYRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGEL
TWGMSVRDCAMLRRSP"
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Aafralvaqclvcvpwdarpppaadsfrqvsclkelvarvlqrlcergaknylafgfa
lldgarggppeafttsvrsylpntytdalrgsgawglllrrygddvlyhllarcalfy
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Homo sapiens telomerase reverse transcriptase (TERT) gene, partial
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Morin,G.B., Carlos,R. and Adams,R.R.
Morin,G.B., Carlos,R. and Adams,R.R.
Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
Location/Qualifiers
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15332)
Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Hann, S.R.,
Adman, R.K., Lichtsteiner, S., Chin, L., Mornin, G.B. and Depinho, R.A.
Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation
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join(13502. .13720,13825. .>15178)
/gene="TERT"
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protein_id="AAD24464.1"
db_xref="GI:4580663"
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/gene="TERT"
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Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0;
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AF121948.1 GI:4580662
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/gene="TERT"
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Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
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                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

(Dassa 1 to 4356)
Cong, Y.S., Wen, J. and Bacchetti, S.
The human telomerase catalytic subunit hTERT: organization of the promoter
Hum. Mol. Genet. 8 (1), 137-142 (1999)
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protein_id="AAD12057.1"
'db_xref="GI:4210971"
               /gene="TERT"
/gene="TERT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-OCT-1998) Pathology, McSt. W., Hamilton, ON L8N 325, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 4356)
Cong,Y.S., Wen,J. and Bacchetti,S.
Direct Submission
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/organism="Homo sapiens"
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/db_xref="texon:9606"
/db_cresone="5"
/db_xref="texon:9606"
/db_xref="texon:9606"
/db_xref="texon:9606"
/gene="TERT"
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/gene="TERT"
join(<3997. .
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Matches 397; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%; Pred. No. 2.38-49;
Conservative 0; Mismatches 0; Indels
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Schiff J.M.
Glycosyltransferase vectors for treating cancer
Patent: US 6713055-A 1 30-MAR-2004;
Location/Qualifiers
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AX453025.1 GI:21712594
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/mol_type="genomic DNA"
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Homo sapiens
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nes 397; Conserv
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Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0;
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1 (bases 1 to 15418)
Gold, J.D. and Lebkowski, J.S.
Methods for providing differentiated stem cells
Patent: US 6576464-A 1 10-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 gcgcacgragaaagcccraaccccagaccaccccaga 397
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Sequence 1 from patent US 6576464.
AR342806
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/mol_type="genomic DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              GATTCGCGGGCACAGACGCCCCAGGACCGCCTTCCCACGTGGCGGAGGGACTGGGGACCC
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                                                                                           GATTCGCGGGCACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACCC
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Geron Corporation (US)
Location/Qualifiers
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Sequence 1 from Patent WO0242468.
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Chimeric cytolytic viruses for cancer treatment
Patent: WO 0203760-A 111-JUL-2002;
Geron Corporation (US)
Location/Qualifiers
Gold,J.D. and Lebrowski,J.S.
Differentiated cells sultable for human therapy
Patent: WO 024245-A 1 30-MAY-2002;
Geron Corporation (US)
Location/Qualifiers
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100.0%; Pred. No. 2.3e-49.
:ive 0; Mismatches 0
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RAPERATGLEGALSGTRHENBYGRQHHAGPPSTSRPPRPWITPCPPVYAETHHFLYS
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15 Londono-Vallejo,J.A.

16 Londono-Vallejo,J.A.

17 Londono-Vallejo,J.A.

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10 Submitted (10-0CT-2010) Centre d'Etudes du Polymorphisme Humain, 27

10 Londono-Vallejo,J.A.

11 Submitted (10-0CT-2011) Centre d'Etudes du Polymorphisme Humain, 27

18 Londono-Vallejo,J.A.

19 Sequence update by submitter

10 Cartion/Qualifière

11 J2564

12 J2564

13 Cartion/Qualifière

14 J2564

15 Cartion/Qualifière

16 J2564

17 Cartion/Qualifière

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18 J2564

J2664

J26
                                                                                                     AX007685 92564 bp DNA linear PRI 22-FEB-2002 Homo mapiens telomerase catalytic subunit (TERT) and sodium channel-like protein genes, complete cds.
                                                      CCTTTCCGCGCCCCCCCTCTCCTCGCGCGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The human telomerase gene: complete genomic sequence and analysis of tandem repeat polymorphisms in intronic regions Oncogene 21 (5), 769-777 (2002)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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24165 GATTCGCGGGACAGACGCCCAGGACCGCGTTCCCACGTGGCGGAGGAACTGGGGACCC 24224
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Center Project Name: 451340
Center clone name: RPCI-11_117B23
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AC114955.1 GI:19424416
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66387. .6661
/rpt_type=dispersed
66661. .66736
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E Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 161252)
Sequencing of Human Chromosome 5
Sequencing of Human Chromosome 5
Unpublished

2. (Dases 1 to 161252)
Direct Submission
Direct Submission
List (14-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute Consensus quality: 148939 bases at least Q40
Consensus quality: 156608 bases at least Q30
Consensus quality: 156608 bases at least Q30
Consensus quality: 158626 bases at least Q30
Consensus quality: 158826 bases at least Q30
Consensus quality: 158826 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 175000; bases; sum-of-contigs estimation
Quality coverage: 7.26 in Q20 bases; sum-of-contigs estimation
\* NOTE: This is a 'working draft' sequence. It currently
\* consists of 9 contigs. The true order of the pieces
\* is not known and their order in this sequence record is
\* arbitrary. Gaps between the contigs are represented as
\* runs of N, but the exact sizes of the gaps are unknown.
\* This record will be updated with the finished sequence
\* as soon as it is available and the accession number will AC114955 161252 bp DNA linear HTG 14-MAR-2002 Homo sapiens chromosome 5 clone RP11-117B23, WORKING DRAFT 24405 GCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGG 24441 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN. Homo sapiens (human)

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Direct Submission
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1 (bases 1 to 20236)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 397; DB 2; Length 161252; 100.0%; Pred. No. 1e-49; tive 0; Mismatches 0; Indels 0;
  1 3008: contig of 3008 bp in length
3109 9209: contig of 6101 bp in length
310 9209: gap of unknown length
9209: gap of unknown length
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15713: gap of unknown length
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3344 39674: contig of 16313 bp in length
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9775 60001: contig of 20227 bp in length
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Homo sapiens
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Best Local Similarity 100.
Matches 397; Conservative
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Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 202305)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submission
Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 15, 2003 this sequence version replaced gi:19224940.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="NOTE: BAC and subclones unstable 76080. Force join
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Best Local Similarity 100.0%; Pred. No. 9.5e-50;
Matches 397; Conservative 0; Mismatches 0; Indels 0;
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DOE Joint Genome Institute.
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PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGGOSWAHPCRTRGPSDRGFCVVSPA
RPAEBATSLBGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETRHFLYS
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LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV
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                                                    Takakura, M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
Direct Submission
Submitted (04-AUG-1998) Masahioro Takakura, Kanazawa University,
School of Medicine, Department of Obstetrics and Gynecology: 13-1,
Takaramachi, Kanazawa, Ishikawa 920-0934, Japan
(E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVAPSCAYOVCGPPLYOLGAATOARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
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Pred. No. 5.6e-49;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       3331. .3336
/note="telomerase transcriptase promoter"
                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=experimental
join(3415. .3633,3738.
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                                                                                                                                                                                                                                                                                                Location/Qualifiers
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3338. .3633
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Best Local Similarity 99.7%;
Matches 396; Conservative (
                                                                                                                                                                                                                                                                       Fax:81-76-234-4266)
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                                                                                                                                                                                                                                                                                          Wick,M. and Hagen,G.
Regulatory dna sequences of the human catalytic telomerase sub-unit gene, diagnostic and therapeutic use thereof
Patent: WO 9933998-A i 08-JUL-1999;
WICK MARSA (DE) BAYER AG (DE)
Location/Qualifiers
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cds.
PAT 24-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primatee; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 395.4; DB 6; Length 5126;
Pred. No. 5.8e-49;
0; Mismatches 1; Indels 0;
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    .5126
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

AX003120 5126 bp Sequence 1 from Patent W09933998.
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Homo sapiens (human)
Homo sapiens
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                                                                                      AX003120.1 GI:9926982
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                                                                                                                                           Homo sapiens (human)
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LOCUS

Search completed: April 9, 2005, 07:02:06 Job time: 1999.42 secs

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April 9, 2005, 04:29:03; Search time 256.83 Seconds (without alignments) 5647.064 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abs98659 Human TER	Abk12706 Human tel	Abv75307 Telomeras	Abv75306 TERT mini	Abz23897 TERT mini	Adi33422 Human tel	Abs98580 Ar17pAE2f	Aax88272 Human cat	Abk12707 Minimal t	Aas96607 DNA encod	Acc47272 CEA gene	Abs98658 Human TER	Adr73423 Human tel	Adr73427 Human m-h	Aah41091 Telomeras	Aaa63785 Nucleotid	Aal38601 Human TER	Abs54997 Lambda cl	Aal38595 DNA of pl	Adc21253 Lambda cl
SUMMARIES	αI	ABS98659	ABK12706	ABV75307	ABV75306	ABZ23897	ADI33422	ABS98580	AAX88272	ABK12707	AAS96607	ACC47272	ABS98658	ADR73423	ADR73427	AAH41091	AAA63785	AAL38601	ABS54997	AAL38595	ADC21253
	DB	9	9	æ	æ	2	12	9	~	9	9	æ	g	13	13	4	m	9	9	φ	2
	* Query Match Length DB	245	261	295	295	295	455	955	5126	5928	51552	378	397	408	902	3962	15418	15418	15418	15418	15418
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Aal55438 Specific	Adi80429 Anti-tumo	Aal55435 Specific	Abq76069 Anticance	Aaa94134 Telomeras	Abz23898 Telomeras	Adn00285 Tumour-sp	Aad27972 Recombina	Aad27971 Recombina	Abs98583 Ar17pAE2f	Aav16979 Human tel	Aad27973 Human tel	Abl92335 Chemicall	Aad22344 Chemicall		Abl92334 Chemicall	Abv73905 Telomeras	Abv74896 Minimal t	Abz79851 Human sit	Abz22591 Human TER	Aad22343 Chemicall	Abq52497 Oligonucl	Abq52496 Oligonucl	Abz20967 Animal te	Add17080 Mouse ula
AAL55438	AD180429	AAL55435	ABQ76069	AAA94134	ABZ23898	ADN00285	AAD27972	AAD27971	ABS98583	AAV16979	AAD27973	ABL92335	AAD22344	ABZ79850	ABL92334	ABV73905	ABV74896	ABZ79851	ABZ22591	AAD22343	ABQ52497	ABQ52496	ABZ20967	ADG37080
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237.4	237.4	236	236	229.8	205	205	201.2	201.2	200.8	199.8	198	183.2	158.6	144	89	88	77	77	77	69.4	67	67	8.99	9.99
21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

BP

ABS98659 standard; DNA; 245

RESULT 1 ABS98659

Virus, viral vector; adenoviral nucleic acid backbone; breast cancer; inverted terminal repeat; ITR; termination signal sequence; lung cancer; ESF responsive promoter; adenoviral packaging signal; prostate cancer; neoplastic condition; colon cancer; cytostatic; immunostimulant; gene therapy; human; TERT; promoter; ds. Recombinant viral vector comprising an adenoviral nucleic acid backbone, useful for treating neoplastic disorders such as lung, breast, prostate Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM; Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S; Police SR, Clarke L, Phipps S, Cheng C; Human TERT promoter sequence #2. 23-FEB-2001; 2001US-0270922P. 01-JUN-2001; 2001US-0295037P. 14-JAN-2002; 2002US-0348670P. 22-FEB-2002; 2002WO-US005300. (NOVS ) NOVARTIS PHARMA AG (first entry) WPI; 2002-706950/76. or colon cancer. WO200267861-A2. Homo sapiens. 17-DEC-2002 06-SEP-2002. ABS98659; 

The present invention relates to a new recombinant viral vector

Claim 11, Page 21, 226pp; English.

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misc_feature
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comprising an adenoviral nucleic acid backbone, where the backbone comprises in sequential order, a left inverted terminal repeat (ITR), a termination signal sequence, an EZF responsive promoter which is operably linked to a gene essential for replication of the recombinant viral vector, an adenoviral packaging signal and a right ITR. The methods and compositions of the present invention are useful for treating a neoplastic condition such as lung, breast, prostets or colon cancer. The viral vectors are useful in studying methods of killing neoplastic cells in vitro or in animal models. The present nucleic acid sequence represents a human TERT promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn; repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer; acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis; skin rejuvenation; immune senseence; bone marrow transplant; skin graft; neoplastic disease; TERT minimal promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCCTCCTCCGCGCGGGACCCCGCCCGGACCCCTCCCGGGTCCCCGGGCCCAGCCC 120
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/note= "A portion of the 5' untranslated region"
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note= "Specifically claimed in claim 37"
190. .202
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/note= "Specifically claimed in claim 37"
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/label= Target_site_C_domain
/note= "Specifically Claimed in claim 37"
182. .259
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                                                                                                                                                                                                                                           Sequence 245 BP; 18 A; 127 C; 66 G; 34 T; 0 U; 0 Other;
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4.5e-34;
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/note= "Repressor site"
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Best Local Similarity 100.
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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system telomerase reverse transcriptase (TERT) from a TERT expression system controlled a TERT promoter and a Site C repression site. The method of the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is useful for modulating expression of TERT for production of reagents contibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents for use in life science research, therapeutic applications, and therapeutic applications, and cally an actual telomeric shortening and/or increasing TERT expression delays natural telomeric shortening and/or increases telomeric length and cells useful for treating disease conditions such as Progeria or Hutchinson-conditions such as Progeria or Hutchinson-conditions such as Progeria or Hutchinson-conditions and cannot be employed to lengthen telomeres of immune senseconce. The method can be employed to lengthen telomeres of osteoblast and osteoclast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and cannet thus be useful to bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of bone carrival and effectiveness of bone carrival and effectiveness of contraining cellular proliferative disease conditions, including conditions e.g. cancer. The present nucleic acid inconting the number of invention is sequence of the
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/note= "E2F transcription factor binding site consensus
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Best Local Similarity 100.0%; Pred. No. 4.4e-34;
Matches 245; Conservative 0; Mismatches 0; Indels (
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/note= "Specifically claimed in claim 37"
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                                                                                                                                                           sequence, E2F-Q6"
192. .201
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05-OCT-2000; 2000US-0238345P.
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191. .201
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CGAGTITCAGGCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 240
                                  194 CGAGTTTCAGGCAGCGCTGCTGCTGCTGCTGGGGAAGCCCTGGCCCCGGCCACCC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor binding site, useful in regulating TERT expression and for screening agents that modulate TERT transcription repressing activity of the TF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TERT; telomerase reverse transcriptase; TF-8; TF-13; telomerase;
cardiovascular; osteopathic; virucide; transcription; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 245; DB 8;
; Pred. No. 4.3e-34;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents the telomerase minimal promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telomerase minimal promoter seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example, Page 31; 40pp, English.
                                                                                                                                                                                                                                                                                                                                                           ABV75307 standard; DNA; 295 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SIER-) SIERRA SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-103520/09.
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                                                                                                                             CCGCG 245
                                                                                                                                                                                           254 CCGCG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agents that modu
and TF-13 sites,
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The invention relates to a new telomerase reverse transcriptase (TERT) TP and/or TF-13 repressor binding site. The nucleic acid comprising the binding site sequence is useful in preparing constructs, such as vectors and expression systems, and probes for the TERT TF-8 and/or TF-13 repressor binding site in non-human animals. Modulating the transcription repressor binding site in non-human animals. Modulating the transcription repressing activity of TERT TF-8 and/or TF-13 repressor factors to regulate telomerase expression, can be used in immortalization of cells, production of reagents useful in life science research, and therapeutic research. Inhibitors of TERT transcription repression by a TF-8 and/or TF-13 repressor may be used for increasing the proliferative capacity of a cell, and for treating Progeria, Hutchinson-Ciliford syndrome.
 215
                                      240
                                                           CGAGTTTCAGGCACCCTGCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor binding site, useful in regulating TERT expression and for screening agents that modulate TERT transcription repressing activity of the TF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCTTCACCTTCCAGCT
                                      CGAGTTTCAGGCAGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC
cercessecerecessecerecerrecerrecersesses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disease, osteoporosis, or AIDS. The present sequence represents the TERT minimal promoter
                                                                                                                                                                                                                                                                                                                                                                                                             дв.
                                                                                                                                                                                                                                                                                                                                                                                          TERT; telomerase reverse transcriptase; TF-8; TF-13; repressor; cardiovascular; osteopathic; virucide; transcription; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 245; DB 8; 100.0%; Pred. No. 4.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 28; 40pp; English.
                                                                                                                                                                                                                                              ABV75306 standard; DNA; 295 BP
                                                                                                                                                                                                                                                                                                                                                         TERT minimal promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001; 2001US-0289717P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37-MAY-2002; 2002WO-US014720.
                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SIER-) SIERRA SCI INC.
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                                                                                                               CCGCG 245
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                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                     07-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews WH;
                                                                                                                                                                                                                                                                                ABV75306;
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9 92 CGGCTCCTCCGCGCGGGACCCCGGCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC 155

CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCCTTCACCTTCAGCT CCGCCTCCTCCGCGCGCGCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGGCCCAGCCC

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CCCCACGTGGCGGAGGGACTGGGGAACCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCT

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36 CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCTCCTCCAGCT
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                     120
                                     96 CGGCCTCCTCGGGGGGACCCGGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCCAGCC 155
                                                                               180
                                                                                                            215
                                                                                                                                         CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGGCCACCC 240
                                                                                                                                                                    275
                                                                                                                                                                                                                                                                                                                                                                                                                       TERT; telomerase reverse transcriptase; promoter; cytostatic; anti-HIV; osteopathic; dermatological; gene therapy; transcription factor; {\it TF}_i cardiant; human; ds.
                                                                                              156 CCTCCGGGCCCTCCCAGCCCTCCTTTCCGCGGCCCCCCCTCTCGCGCGC
                                                                                                                                                         216 CGAGTTTCAGGCAGCGCTGCGCCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid having a nucleotide sequence that is identical to a telomerase reverse transcriptase (TERT) activator-binding site in the minimal TERT promoter useful for treating cellular proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 245; DB 10; Length 295; 100.0%; Pred. No. 4.3e-34; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 45; 60pp; English.
                                                                                                                                                                                                                                                                                                           ABZ23897 standard; DNA; 295 BP.
                                                                                                                                                                                                                                                                                                                                                                                                TERT minimal promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2001; 2001US-0289641P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-2002; 2002WO-US014740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, e.g. cancer, AIDS.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  18-MAR-2003
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                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                      ABZ23897;
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This invention relates to a novel polynucleotide comprising a human telomerase promoter and at least one viral El gene. Specifically, the genes are BlA, IRES and ElB and the human telomerase promoter is preferably high. The present invention describes a virus containing this polynucleotide and an anticancer agent that replicates efficiently in tumour cells and causing cell death. As such, it can be used for the treatment of cancer, in particular cancer of the stomach, large intestine, lung, liver, prostate, pancreas, digestive tract, bladder, mammary gland, uterus, thyroid gland and ovary. Accordingly, this composition exhibits cycostatic activity. This polynucleotide sequence is the human telomerase promoter (HTERT) DNA of the invention.
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                                                                                                                                   CCGCCTCCTCCGCGCGCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC
                 CGGCTCCTCGGGGGGGGGACCCGGCGCGCGTCCCGACCCTCCCGGGTCCCCGGGCCCAGCCC
                                                          CGAGITITCAGGCAGCGCTGCTGCTGCACGTGGGAAGCCCTGGCCCCGGCCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                 telomerase promoter; human; El; ElA; IRES; ElB; anticancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide comprising a human telomerase promoter and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 455 BP; 41 A; 212 C; 142 G; 60 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                        Human telomerase promoter (hTERT) DNA SeqID 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KANS-) KANSAI TECHNOLOGY LICENSING ORG
(FUJI/) FUJIWARA T.
(TANA/) TANAKA N.
(KYOS/) KYO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 4; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    cell death; cancer; cytostatic; ds.
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                                                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                   ADI33422 standard; DNA; 455
                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-099391/10.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                              22-APR-2004
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al Similarity 100. 245, Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising an adenoviral nucleic acid backbone, where the backbone comprises in sequential order, a left inverted terminal repeat (ITR), a termination signal sequence, an E2F responsive promoter which is operably linked to a gene essential for replication of the recombinant viral vector, an adenoviral packaging signal and a right ITR. The methods and compositions of the present invention are useful for treating a
                                       270
                                                                                                                      390
                                                                                                                                                             CGAGTTTCAGGCAGCGCTGCGTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 450
                     9
                                                                                                                                                                                                                                                                                                                                                         inverted terminal repeat; ITR; termination signal sequence; lung cancer; E2F responsive promoter; adenoviral packaging signal; prostate cancer; neoplastic condition; colon cancer; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant viral vector comprising an adenoviral nucleic acid backbone, useful for treating neoplastic disorders such as lung, breast, prostate
                                                                                                  CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGCGAAGCCCTGGCCCGGGCACCC
                                                           CCGCCTCCTCCGCGCGGGACCCCGGCCCGGACCCCTCCCGGGTCCCCGGCCCAGCCC
                                                                        CGGCCTCCTCCGCGGGGGACCCCCCCCCCCCGACCCCTCCCGGGGTCCCCGGGCCCAGCCC
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                    CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCTTCACCTTCCAGCT
                               CCCCACGTGGCGGAGGGACTGGGACCCGGCCCCTCCTGCCTTCACCTTCAGCT
                                                                                                                                                                                                                                                                                                                                                Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
 Gaps
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JL, Kaleko M, Ryan PC, Stewart DA,
, Clarke L, Phipps S, Cheng C;
                                                                                                                                                                                                                                                                                                                            Arl7pAE2fFTrtex right end viral DNA sequence.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001; 2001US-0295037P.
                                                                                                                                                                                                                                                      ABS98580 standard; DNA; 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVS ) NOVARTIS PHARMA AG.
                                                                                                                                                                                                                                                                                                        (first entry)
245; Conservative
                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-706950/76.
                                                                                                                                                                                 CCGCG 245
                                                                                                                                                                                                     CCGCG 455
                                                                                                                                                                                                                                                                                                                                                                                        therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200267861-A2.
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17-DEC-2002
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                                                                              271
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                                                                                                                                                                                                                                                                           ABS98580;
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                                                                                                                                                                                                                                                                                                                                                                                                          Viruses.
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ABS98580/c
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                                                                                                                                                                                                                                                                                                                                                                               441
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neoplastic condition such as lung, breast, prostate or colon cancer. The viral vectors are useful in studying methods of killing neoplastic cells in vitro or in animal models. The present nucleic acid sequence represents a viral DNA sequence that was used in the methods of the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCCTCCTCCGCGCGCGCCCCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGGCCCAGCCC
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                                                                                                                                                                                                                100.0%; Score 245; DB 6; Length 955; 100.0%; Pred. No. 3.6e-34; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telomerase, subunit, human, regulatory, catalytic, anti-tum
modulator, telomerase regulatory region, cancer therapy; ss
                                                                                                                                                                 Sequence 955 BP; 266 A; 286 C; 236 G; 167 T; 0 U; 0 Other;
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Matches 245, Conservative
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/note= "Ampicillin Resistance Gene, made sensitive by
                                                                             CCGCCTCCTCCGCGCGCGCCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC
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                                                   Gaps
                  Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;
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/note= "Secreted Alkaline Phosphatase gene"
1860. .2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "PolyA addition site"
/note= "Late Poly-A addition site of SV40"
2394. .2976
                                                                                                                                                                                                                                                                                                                 Minimal telomerase promoter in plasmid designated pSSI20.
                                                  Indels
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/note= "Chloramphenicol Resistance Gene"
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/note= "Bacterial origin of replication"
3170. .4023
                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "Telomerase minimal promoter"
                                                   0
                                  100.0%; Score 245; DB 2; 100.0%; Pred. No. 2.8e-34;
                                                  0; Mismatches
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/note= "Kozak fragment"
308. .1864
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Synthetic.
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The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repression system can that includes a TERT promoter and a Site C repression repression by the Site C repression invention involves modulating TERT transcription repression by the Site C repression of TERT for producing a mammalian can the Site C repression of TERT for producing a mammalian of useful for modulating expression of TERT for producing a mammalian can therefore, including immortalisation of cells, production of reagents of presents applications, including immortalisation of cells, production of reagents cremening amortalisation of cells, production of reagents contenting and or increases telomeral length and cells applications in such that severe solution and cells and such as Progeria or Hutchinson-cells syntame senses relomeration and to inhibit immune sensescence. The method can be employed to lengthen telomeres of osteoblast and osteoclast stem cells, encouraging bone replacement and osteoclast stem cells, encouraging bone replacement and can as such the method improves the survival and effectiveness of bone marrow and skin cell transplants. Generally and relations contains such the method improves the survival and effectiveness of bone marrow and skin cell transplants. Decreasing TERT expression is useful for treating cellular proliferative disease conditions, including cequence represents plasmid SSI20 minimal telomerace promoter sequence. This sequence contains part of the human. TERT minimal promoter sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding
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; Pred. No. 2.7e-34;
0; Mismatches 0; Indels 0.
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/*tag= h
/note= "F1 Origin of Replication"
5768. .5921
                                                                                                                                     'note= "Transcription blocker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 2; 66pp; English.
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01-SEP-2000; 2000US-0230174P.
05-OCT-2000; 2000US-0238345P.
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Best Local Similarity 100.
Matches 245; Conservative
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New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell growth.
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31273. .31358
//ttag= p
3/3399. .33843
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3/3844. .33957
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//number= g
3/3844. .39591
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07-DEC-2000; 2000US-00733294
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P-PSDB; AAU72735.
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  CGAGITICAGGCAGCGCTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACC 240
                        Telomerase reverse transcriptase, TERT, cytostatic, apoptosis, cell growth inhibitor, antisense oligonucleotide, antisense technology,
                                                                                                                                                                                                    DNA encoding human telomerase reverse transcriptase (TERT) #1.
                                                                                                                                                                                                                                                                                                                                              product= "TERT"
note= "Telomerase reverse transcriptase"
1493. .11596
*tag= c
                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .11492
                                                                                                                                  AAS96607 standard; DNA; 51552 BP.
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11274. 47813
(*tag= b
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30293. .31272
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22-FEB-2002; 2002WO-US005300
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                         WPI; 2003-256488/25.
                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                   of the CEA gene
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Fang B;
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Matches
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                      The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridises with and inhibits the expression of TERT. A series of oligonucleotides were conclections in length and composed of a central gap region consisting of the 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-KMS) nucleotide wings. The wings were composed for their effect on human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PGR). The compound is useful for inhibiting the expression of TERT in calls or tissues, for reacting a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell growth (preferably, cancer cell growth), in antisense therapy and for creares transcriptase (TERT) #1, sequence encodes human telomerase reverse transcriptase (TERT) #1, and is used to create antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11089 CCGCCTCCTCCGCGCGGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC 11148
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                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pression; promoter; cytostatic; gene therapy; antisense therapy; cis-acting; CEA gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                       1 CCCCACGTGGCGGAGGGACTGGGGACCCGGCACCCGTCCTGCCCTTCACCTTCCAGCT
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                   Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                 Length 51552;
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 245; DB 6; 100.0%; Pred. No. 1.9e-34;
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
  Example 19; Page 112-138; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC47272 standard; DNA; 378 BP.
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                                                                                                                                                                                                                                                                                                                                                            245; Conservative
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression;
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                                                                                                                                                                                                                                                                             the invention
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Matches ;
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preferential manner. The method involves providing a first expression
cassette having a cell type-preferential promoter, providing a second
expression cassette having an inducible promoter, and transferring the
first and second expression cassettes into a cell in which the cell type
specific preferential promoter is active. The methods and compositions
of the present invention are useful for treating cancers of the brain,
head and neck, esophagus, thyroid, stomach, colon, liver, kidney,
prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The
Expressing gene products in a cell type-preferential manner with a binary or bicistronic expression system, useful for treating cancers of the brain, head and neck, esophagus, thyroid, stomach, colon, liver, prostate, skin and rectum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 cerecegecerecensecerecerrecerrecesesecececererereses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 CCCCACGTGGCGAAGGAACTGGGGACCGGGCACCGTCCTGCCCTTCACCTTCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 244; DB 8; 100.0%; Pred. No. 6.2e-34; ive 0; Mismatches 0;
                                                                                                                                                                                                         Disclosure; Page 139; 141pp; English.
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                                                                                                                                                                                                                                                    The present invention relates to a new recombinant viral vector comprising an adenoviral nucleic acid backbone, where the backbone comprises in sequential order, a left inverted terminal repeat (ITR), a termination signal sequence, an B2F responsive promoter which is operably linked to a gene essential for replication of the recombinant viral vector, an adenoviral packaging signal and a right ITR. The methods and compositions of the present invention are useful for treating a neoplastic condition such as lung, breast, prostate or colon cancer. The viral vectors are useful in studying methods of killing neoplastic cells in vitro or in animal models. The present nucleic acid sequence represents a human TERT promoter of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                        Recombinant viral vector comprising an adenoviral nucleic acid backbone, useful for treating neoplastic disorders such as lung, breast, prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 CCCACGTGGCGGAGGACTGGGGACCCGGGCACCCTTCTCTTCACCTTCCAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human telomerase reverse transcriptase (hTERT) gene promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCTC
                                                                                          Hallenbeck PL, Hay CM; Y, Xie Y, Connelly S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds, cytostatic; gene therapy; transcriptional regulatory sequence; human telomere reverse transcriptase; hTERT; promoter; c-Myc binding site; Sp1 binding site; cancer.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 397 BP; 35 A; 186 C; 127 G; 49 T; 0 U; 0 Other;
                                                                                          Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck
Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y,
Police SR, Clarke L, Phipps S, Cheng C;
                                                                                                                                                                                                                            Claim 11; Page 21; 226pp; English.
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           23-FEB-2001; 2001US-0270922P.
01-JUN-2001; 2001US-0295037P.
14-JAN-2002; 2002US-0348670P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR73423 standard; DNA; 408
                                                                (NOVS ) NOVARTIS PHARMA AG.
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                                                                                                                                               WPI; 2002-706950/76
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                                                                                                                                                                                                      colon cancer.
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The invention relates to a transcriptional regulatory sequence with a human telomere reverse transcriptase (hTERT) promoter linked to a nucleotide sequence comprishing one or more c-Myo binding sites and/or one or more Spl binding sites and/or one composition are useful for treating cancer, e.g. stomach, lung, ovarian, liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer. This sequence corresponds to the wild type human telomerase reverse transcriptase (hTERT) promoter sequence used to generate the novel sequence of the
                                                                                                                                                                                                                                                                                                                                                New transcriptional regulatory sequence with a human telomere reverse transcriptase promoter, useful for treating cancer, e.g. stomach, lung, ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 CGCTCCTCCGCGCGGGACCCCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 CCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCTTCACCTTCCAGCTC
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human telomere reverse transcriptase; hTBRT; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 408 BP; 35 A; 190 C; 132 G; 51 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%; Score 244; DB 13;
100.0%; Pred. No. 6.2e-34;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1; 130pp; English.
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                                                  27-FEB-2004; 2004WO-KR000427.
                                                                                                     27-FEB-2003; 2003KR-00012364.
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                                                                                                                                                           (YUNC/) YUN C.
(KIMJ/) KIM J.
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or more Spl binding sites. The transcriptional regulatory sequence and composition are useful for treating cancer, e.g. stomach, lung, ovarian, liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder, colon, cervical, breast, brain, or head and neck cancer. This sequence corresponds to the modified human telomerase reverse transcriptase (hTERT) promoter sequence containing the extra c-Myc and Spl binding site
                                                                                                           Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;
                                                                                      sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transcriptional regulatory sequence with a human telomere reverse transcriptase promoter, useful for treating cancer, e.g. stomach, lung, ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
                                                                                                                                                                                                                                                                                      /*tag= f
/bound_moiety= "Spl transcription factor"
381. .386
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bound moiety= "Sp1 transcription factor"
:50. .255
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bound moiety= "Sp1 transcription factor"
102. .310
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31. .336
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'bound moiety= "Sp1 transcription factor"
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/note= "translation start site"
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128. .236
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bound moiety= "c-Myc protein"
72. .680
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'bound moiety= "c-Myc protein"
117. .622
         site; cancer
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(KIMJ/) KIM J.
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Yun C,

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Isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants, useful e.g. in gene localization and classification analysis.
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99.6%; Score 244; DB 13;
100.0%; Pred. No. 5.4e-34;
ive 0; Mismatches 0;
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3742 GGCTCCTCCGCGGGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCC 3801
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                                                                                                                                                                                                                                                                                                                                                                                                    182 GAGTITCAGGCAGCGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCC 241
classification analysis, studying gene development networks and function networks, and designing drugs based on regulatory sequences of the phenotypes for disease treatment. The present sequence represents BNA encoding a telomere reverse transcriptase (TERT), which is used in an example illustrating the use of the method of the invention
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rative 0; Mismatches 0; Indels
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Sequence 12197, A
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                Sequence
Seq
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US-09-165-264-12

US-09-165-264-11

US-09-90-016-16972

US-08-232-463-14

US-08-128-155-16

US-08-912-951-4

US-08-912-951-4

US-09-9402-181B-4

US-09-9402-181B-4

US-09-721-456-4

US-09-851-843A-224

US-08-851-843A-24

US-09-872-423B-3

US-09-572-423B-3

US-09-672-423B-3

US-09-672-321-1

US-09-672-321-1

US-09-672-321-1
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                   Sequence 25, Application US/09932581

Sequence 25, Application US/09932581

Patent No. 6686159

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Praser, Stepher A.

APPLICANT: Praser, Stepher A.

APPLICANT: Mohammadpour, Hanid

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)

CURRENT APPLICATION NUMBER: 60/29/32,581

CURRENT APPLICATION NUMBER: 60/227,865

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/238,345

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01
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100.0%; Score 245; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.8e-41;
Matchos 245; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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254 CCGCG 258
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US-09-949-016-12197
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LENGTH: 5928
                                                               RESULT 2
US-09-932-581-25
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US-09-949-016-17583

US-09-949-016-17583

Sequence 17583, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FEASTSEQ for Windows Version 4.0

SEQ ID NO 17883

LENGTH: 44960

TURED TO NO 17883
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                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 245; DB 4; Length 44952; 100.0%; Pred. No. 2.7e-41; tive 0; Mismatches 0; Indels 0;
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100.0%; Score 245; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOSTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12197

LENGTH: 44952

TYPE: DNA

TYPE: DNA

CRANISM: Human

FEATURE:
NAME/KEY: misc_feature

NAME/KEY: misc_feature

CHARR INFORMATION: n = A,T,C or G

US-09-949-016-12197
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// LOCATION: (1)...(44960)

// OTHER INFORMATION: n = A,T,C or

US-09-949-016-17883
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1 CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCGTCCTGCCCTTCACCTTCCAGCT
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100.0%; Score 245; DB 4; Length 51552;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 1010101 IN NAME/KEY: exon LOCATION: (37885)...(38073) OTHER INFORMATION: exon 11 NAME/KEY: intron LOCATION: (38074)...(41874) OTHER INFORMATION: intron 11 LOCATION: (41875)...(42001) OTHER INFORMATION: exon 12 NAME/KEY: intron LOCATION: (42002)...(42881) OTHER INFORMATION: intron 12 OTHER INFORMATION: intron 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (46130) ... (46254)
OTHER INFORMATION: exon 14
NAME/KEY: intron
LOCATION: (46255) ... (47035)
OTHER INFORMATION: intron 14
NAME/KEY: exon
LOCATION: (47036) ... (47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174) ... (47709)
OTHER INFORMATION: intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: (3594)...(36013)
OTHER INFORMATION: exon 10
NAME/KEY: intron
LOCATION: (36014)...(37884)
OTHER INFORMATION: intron 10
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OTHER INFORMATION: exon 13
NAME/KEX: intron
LOCATION: (42944) ... (46129)
OTHER INFORMATION: intron 13
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: 31450
OTHER INFORMATION: unknown
NAME/KEY: exon
LOCATION: (33844) ... (33957)
OTHER INFORMATION: exon 9
NAME/KEY: intron
LOCATION: (33958) ... (35941)
OTHER INFORMATION: intron 9
                                                                                                                                                          NAME/KEY: exon
LOCATION: (30195) ...(30292)
OTHER INFORMATION: exon 7
NAME/KEY: intron
LOCATION: (30293) ...(31272)
OTHER INFORMATION: intron 7
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; OTHER INFORMATION: exon 16
US-09-733-294A-30
                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (31273)...(31358)
OTHER INFORMATION: exon 8
NAME/KEY: intron
LOCATION: (31359)...(33843)
OTHER INFORMATION: intron 8
                                                                                             LOCATION: (25550)...(30196)
OTHER INFORMATION: intron 6
OTHER INFORMATION: exon 6
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                         1871 CCGCCTCCTCCGCGCGGACCCCGCCCGTCCCGACCCTCCCGGGTCCCCGGCCCAGCCC 1930
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                                                                                                                                                                                                                                                                      sequence 30, Application US/09733294A

sequence 30, Application US/09733294A

parent No. 6492171

GENERAL INFORMATION:

APPLICANT: Bett P. Monia

APPLICANT: Bett P. Monia

APPLICANT: Bedward V. Wancewicz

TITLE OF INFORMATION: ANTISENSE MODULATION OF TERT EXPRESSION

FILE REFERENCE: ISPH-057

CURRENT APPLICATION NUMBER: US/09/73,294A

CURRENT FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-07

PRIOR PILING DATE: 2000-15-16

WOMBER OF SEQ ID NOS: 108

SEQ ID NO 30

LENGTH: 51552
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LOCATION: (24900) ...(25393)
OTHER INFORMATION: intron 5
NAME/KEY: exon
LOCATION: (25394) ...(25549)
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NAME/KEY: exon
LOCATION: (1) ... (11492)
LOCATION: (1) ... (11492)
NAME/KEY: intron
LOCATION: (11493) ... (11596)
OTHER INFORMATION: intron 1
NAME/KEY: exon
LOCATION: (11597) ... (12950)
OTHER INFORMATION: intron 2
NAME/KEY: exon
LOCATION: (12951) ... (21566)
OTHER INFORMATION: intron 2
NAME/KEY: exon
LOCATION: (12951) ... (21566)
OTHER INFORMATION: intron 2
NAME/KEY: exon
LOCATION: (2267) ... (21762)
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LOCATION: (21763)...(23851)
OTHER INFORMATION: intron 3
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LOCATION: (23852)...(24032)
OTHER INFORMATION: exon 4
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LOCATION: (24033)...(24719)
OTHER INFORMATION: intron 4
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LOCATION: (24720)...(24899)
OTHER INFORMATION: exon 5
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ORGANISM: Homo sapiens
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LOCATION: 1..4321
OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
                                                                                                                     Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerage Catalytic Subunit NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 015389-002620US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,312
APPLICATION NUMBER: US 08/851,505
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
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COCATION: 4160.4313
OTHER INFORMATION: /note= "in
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-402-1818-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: intron
LOCATION: 2702..2804
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                         Chapman, Karen E
Morin, Gregg B.
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
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APPLICANT: Morin, Gregg B.
APPLICANT: Lichtereiner, Serge
APPLICANT: Adams, Robert R.
APPLICANT: Geron Corporation
ITLE OF INVENTION: Regulatory Sequences and Methods of Using
FILE REPERENCE: 109/246P
CURRENT APPLICATION NUMBER: US/09/244,438
CURRENT FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 298
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; OTHER INFORMATION: Human TERT promoter
US-09-244-438-17
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Patent No. 6610839
GENERAL INFORMATION:
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US-09-244-438-17
Sequence 17, Application US/09244438
; Patent No. 6777203
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ORGANISM: Homo sapiens
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US-09-402-181B-6
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GENERAL INCORMATION:
APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVERTURE GLOSSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
LENGTH: 15418
                                                               ; Sequence 1, Application US/0999427A; Patent No. 6713055
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LENGTH: 15418
                                               US-09-994-427A-1
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      Length 4321;
                                                                                  2 CCCACGIGGCGGAGGGACIGGGGACCCGGGCACCCGICCIGCCCTIC
  99.6%; Score 244; DB 4; Length 43
100.0%; Pred. No. 4.4e-41;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09783203
Patent No. 6576464
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Lebkowski, Jane
TITLE OF INVENTION: Tpacked stem cells
TITLE REFERENCE: 096/003
CURRENT FILING DATE: 2001-02-13
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,443
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,357
PRIOR FILING DATE: 2000-11-27
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
SEQ ID NO 1
Query Match
Best Local Similarity 100.
Matches 244; Conservative
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Matches 244; Conservative
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13301 CCCACGTGGCGGAGGACTGGGGACCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCTC 13360
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                                                                                                                                                                Gaps
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APPLICANT: Lichtsteiner, Serge
APPLICANT: Lichtsteiner, Serge
APPLICANT: Lichtsteiner, Alain
APPLICANT: Adams, Robert R.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
TITLE OF INVENTION: Regulatory Sequences and Methods of Using
FILE REFERENCE: 019/246P
CURRENT APPLICATION NUMBER: US/09/244,438
CURRENT FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
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                                                                                                             Length 15418;
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                                                                                                                                                                0; Indels
                                                                                                       99.6%; Score 244; DB 4; L
100.0%; Pred. No. 4.4e-41;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09244438; Patent No. 6777203
                                                                                                       Query Match
Best Local Similarity 100.
Matches 244; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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62 GGCCTCCTCCGGGGGGGGCCCCGGCCCGGACCCCTCCCGGGTCCCCGGCCCAGCCCC 121
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Best Local Similarity 94.7
Matches 233; Conservative
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                                                                                                                    CGCCTCCTCCGCGCGGGGCCCCGGTCCCGACCCCTCCCGGGTCCCCGGGCCCAGCCCC
                                                                                                                                          182 GAGTTTCAGGCAGCGCTGCGTCCTGCTGCACGTGGGAAGCCCTGGCCCCGGGCCACCCC
                                               CCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCTC
              Gaps
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                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence B, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILLE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR PILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOTTWARE: PATENTIN VEY. 2.1
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-912-951-6
; Sequence 6, Application US/08912951
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Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                  13541 ĆĠĆĠ 13544
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US-09-916-510A-8
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2067 cccaccidecesaaccacidesacccesecaccesicercerecectricacerrecacite 2126 APPLICANT: Cech, Thomas R.
APPLICANT: Lingmar, Joachim
APPLICANT: Lingmar, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Andrews, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: THEAPPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS: 61 2 cccaccingccccaccingcaacingcaacccccaccinccinccccritcaccinccaccinc 2; Gaps Length 4200; Indels COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: BREENIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FLING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US 08/854,050
FLING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FRING APPLICATION NUMBER: US 08/851,843
FRING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: (415) 576-0300
INFORMATION FOR SED ID NO: 6: SEQUENCE CHARACTERISTICS:
LEDGTH: 4200 Dass pairs
TYPE: nucleic acid
STRANDEDNESS: aingle 83.4%; Score 204.4; DB 4; 94.7%; Pred. No. 4.5e-33; tive 0; Mismatches 11; ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California STATE: California STATE: Alifornia STATE: 94111

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Query Match
Best Local Similarity 98.5%;
Matches 203; Conservative
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                i LENGTH: 35978
i TYPE: DNA
i ORGANISM: Adenovirus
US-09-956-335-1
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  2127 GGCTTCTTCCGCGGGACCCGGCCCCTCCCGAACCCTTCCCAGGTCCCGGGCCCAGCCCC 2186
                                                                                          2247 GCGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACC 2306
                                                                                                                                                          180 GCGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCTCCTCCGCGCGGGACCCCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCC 121
                                                                     CTCCGGGCCCTCCCAGCCCCTTCC-TTTCCGCGGCCCCGCCCTCTCC-TCGCGGC 179
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09956335

Sequence 2, Application US/09956335

Batent No. 6627190

GENERAL INFORMATION:

APPLICANT: WOLD, William

APPLICANT: WOLD, William

APPLICANT: KUPPASWAMI, Mohan

APPLICANT: KUPPASWAMI, Mohan

APPLICANT: CORPANIANI ADENOVIRUS VECTORS THAT ARE

TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

TITLE OF INVENTION: REPLICATION -COMPETENT IN TERT-EXPRESSING CELLS

TITLE OF INVENTION: REPLICATION -COMPETENT IN TERT-EXPRESSING CELLS

CURRENT APPLICATION NUMBER: US/09/956,335

CURRENT FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH 35871
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APPLICANT: WOLD, William
APPLICANT: TOTH, Kazoly
APPLICANT: TOTH, Kazoly
APPLICANT: WORDANAMI, Mohan
APPLICANT: WORDANAMI, MOHAN
APPLICANT: WORDANAMI, MOHAN
APPLICANT: WORDANAMI, WOHAN
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956,335
CURRENT FILING DATE: 2001-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.1
Best Local Similarity 98.5
Matches 203; Conservative
                                                                                                                                                                                                                                                                                            2307 CCCGCG 2312
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CORGANISM: Adenovirus
US-09-956-335-2
                                                                                                                                                                                                                                                240 CCCGCG 245
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US-09-956-335-1/c
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34219 CTCCGGGCCCTCCCACCCCTCCCTTTCCGCGGCCCCCCCTCTCTCGCGGCGC 34160
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                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                        122 CTCCGGGCCCTCCCAGCCCCTTCCTTTCCGCGGCCCCGCCCTCTCCTCGCGGCGC
                                                                                              2 CCCACGTGGCGGAGGGACTGGGGACCCGGCCACCCGTCCTGCCCTTCACCTTCCAGCTC
                                                    Gaps
    Length 35978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08974549A
; Sequence 6, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Applicant Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
21P.
                                               3, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FALOPY disk
MEDIUM TYPE: FALOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
RRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
RRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
RRIOR APPLICATION NUMBER: US 08/8651,843
APPLICATION NUMBER: US 08/8651,843
Score 201.2; DB 4;
Pred. No. 2e-32;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                  34159 GAGTTTCAGGCAGCGCTGATTACTGC 34134
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2249 CCCACGTGGCGGAGGGACTGGGGACCCGGCACCGGTCCTGCCCCTTCACCTTCCAGCTC 2308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 CCCTCCGGGCCCTCCCAGCCCCTTCC-TTTCCGCGGCCCCGGCCCTCTCCTCGCGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCGCCCTTCCAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: -
LOCATION: 1..4335
OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
FEATURE:
FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AuG-1997

PRIOR APPLICATION NUMBER: US 08/912,951

PRIOR APPLICATION NUMBER: US 08/912,951

PRIOR APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AuG-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

PRIOR APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: APPLICATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REFERRINCE/DOCKET NUMBER: 015389-002610US

TELEPAX: (415) 576-0300

TELEPAX: (415) 576-0300

TELEPAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LEMOTH: 4335 base pairs

TYPE: nucleic acid

STRANDED.SS. single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: intron
LOCATION: 2715..2818
OTHER INFORMATION: /note= "intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: intron
; LOCATION: 4173.4326
; OTHER INFORMATION: /note= "intron 2"
US-08-974-549A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2489 CCCCCC 2495
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Search completed: April 9, 2005, 07:05:40 Job time : 78.8505 secs

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PAT 10-DEC-2003
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AY007685 Homo sapi
AC114955 Homo sapi
AC114955 Homo sapi
AC1257662 Antineopi
BD262062 Antineopi
AR303036 Sequence
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AF22590 Homo sapi
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AR43331 Sequence
AR403723 Sequence
AR403723 Sequence
AR403723 Sequence
AR30041 Sequence
AR30041 Sequence
AR30041 Sequence
AR301041 Sequence
AC122155 Sequence
AC122155 Papio anu
AX365010 Sequence
AR33406 Sequence
AR33466 Sequence
AR33466 Sequence
AR33660 Sequence
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                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     AR455879 Sequence
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/note="A 245 bp fragment of the hTERT promoter"
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Patent: WO 02067861-A 94 06-SEP-2002;
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .245
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Sequence 94 from Patent WO02067861.
AX817858
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AR403724
AR403724
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B36796
AR393087
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AR386012
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AX490405 Sequence
                                                                 April 9, 2005, 05:34:49; Search time 1229.58 Seconds (without alignments) 9654.950 Million cell updates/sec
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                       4708233 segs, 24227607955 residues
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                               nucleic search, using sw model
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AX817781
AR017781
AR016767
AR455897
AX03122
HSTERT1
AR266023
AX817857
AR3999956
AR390473
AR190473
AR191348
AR342896
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AX504952
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Maximum Match 100%
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seg length: 200000000
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Wick,M. and Hagen,G.
Regulatory dna sequences of the human catalytic telomerase sub-unit gene, diagnostic and therapeutic use thereof patent: WO 9933998-A 1 08-UUL-1999; WICK MARESA (DE); BAYER AG (DE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Fig.47. Sequence of the right end
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tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.9e-29;
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    .5126
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Sequence 1 from Patent W09933998
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     181 CGAGTTTCAGGCAGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 240
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1 (bases 1 to 261)

Andrews, W.H., Foster, C.A., Fraser, S. and Mohammadpour, H. Methods and compositions for modulating telomerase reverse transcriptase (TERT) expression
Patent: US 6686159-A 24 03-FEB-2004;
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Best Local Similarity 100.0%; Pred. No. 4.7e-29;
Matches 245; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Viral vector sequence"
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Patent: WO 02067861-A 17 06-SEP-2002;
Location/Qualifiers
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Sequence 17 from Patent W002067861.
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Sequence 24 from patent US 6686159.
AR455896

    261
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    /mol_type="genomic DNA"

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Andrews, W.H., Foster, C.A., Fraser, S. and Mohammadpour, H.
Andrews, and compositions for modulating telomerase reverse
transcriptes (FTT) expression
Patent: US 6686159-A 25 03-FEB-2004;
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                                                                                       Length 5491;
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100.0%; Score 245; DB 6; Length 5
al Similarity 100.0%; Pred. No. 1.5e-29;
245; Conservative 0; Mismatches 0; Indels
                                                                                                                          0; Indels
                                                                                       100.0%; Score 245; DB 9;
100.0%; Pred. No. 1.6e-29;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 from patent US 6686159. AR455897

    .5928
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    /mol_type="genomic DNA"

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5089. .>5491
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                                                                                                                            Matches 245; Conservative
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Cloning of human telomerase catalytic subunit (hTERT) gene promoter
and identification of proximal core promoter sequences essential
for transcriptional activation in immortalized and cancer cells
Cancer Res. 59 (3), 551-557 (1999)
                                                                                                                                мвуць/67
Homo sapiens gene for telomerase transcriptase, partial cds.
AB016767
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WKMSVRDCAMLRRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takakura, M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
Takakura, M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
Direct Submission
Submitsed (04-AUG-1998) Masahioro Takakura, Kanazawa University,
School of Medicine, Department of Obstetrics and Gynecology; 13-1,
Takaramachi, Kanazawa, Ishikawa 920-0934, Japan
                                                                                                                                                                                                                                                                           Bukaryota; Metazoa, Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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telomerase transcriptase, hTERT
Homo sapiens (human)
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Location/Qualifiers
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11089 CCCCTCCTCCGCGCGGGGCCCCGCCCGGCCCGACCCCTCCCGGGTCCCCGGGCCCAGCCC 11148
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Direct Submission
Submitted (16-FEB-199) Dept. of Mol. Biol., Bayer AG Leverkusen,
ZF-BTM, Bldg. Q18, Leverkusen D-51368, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CGGCTCCTCCGCGCGGGACCCCGCCCGTCCCGACCCCTCCCGGGGTCCCCGGGCCCAGCCC
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1 (bases 1 to 51552)

Monia, B.P., Gaarde, W.A., Freier, S.M. and Wancewicz, E. Antieense modulation of TERT expression
Patent: US 6492171-A 30 10-DEC-2002;
Location/Qualifiers
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100.0%; Pred. No. 8.8e-30;
ive 0; Mismatches 0;
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Matches 245; Conservative
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                                                                                                                                                                                                                                                Wick,M. and Hagen,G.
Regulatory dna sequences of the human catalytic telomerase sub-unit gene, diagnostic and therapeutic use thereof
Patent: WO 993399-A 3 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
Location/Qualifiers
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                                                                                     PAT 24-AUG-2000
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Homo sapiens telomerase reverse transcriptase (TERT) gene, exons
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(Dases 1 to 26414)

Wick,M., Zubov,D. and Hagen,G.

Mick,M., Zubov,D. and promoter characterization of the gene encoding the human tolomerase reverse transcriptase (hTERT)

Gene 232 (1), 97-106 (1999)
                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                     linear
                                                                                   DNA
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Sequence 3 from Patent WO9933998.
                                                                                                                                  AX003122.1 GI:9926984
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AF128893.1 GI:4808970
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2 (bases 1 to 26414)
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Homo sapiens
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Matches 245, Conservative
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 291 CCGCG 295
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2043 bp DNA linear PRI 05-FEB-1999 Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter region and partial cds.
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| Da xref="GG1:4226058"
| translation="WPRAPRCRAVESLIRSHYREVLPLATFVRRLGPQGWRLVQRGDP
| AAFRALVAQCLVCVPDARPPPAAPSFRQ"
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Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.
Direct Submission
Submitted (15-0CT-1998) Laboratory of Molecular Carcinogenesis,
National Institute of Environmental Health Sciences, 111 T. W.
Alexander Drive, P.O. Box 12233, Research Triangle Park, NC 27709,
USA
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2043)
Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.
Cloning and characterization of the promoter region of human
talomerase reverse transcriptase gene
Cancer Res. 59 (4), 826-830 (1999)
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/codon_start=1
product="telomerase reverse transcriptase"
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100.0%; Pred. No. 3.2e-29;
tive 0; Mismatches 0;
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1. .2043
/organism="Homo sapi
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/gene="TERT"
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gene="TERT"
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/gene="TERT"
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Matches 244; Conservative
                     CGCC 245
                                                      394 CGCG 397
                   242
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                     Length 51552;
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100.0%; Score 245; DB 6;
Best Local Similarity 100.0%; Pred. No. 6.9e-30;
Matches 245; Conservative 0; Mismatches 0;
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Patent: WO 02067861-A 93 06-SEP-2002;
Location/Qualifiers
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Sequence 93 from Patent W002067861.
AX817857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
1. .397
1. .51552
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/mol_type="genomic DNA"
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AX817857
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/product="telomerase reverse transcriptase"
/protein id="AAD12057.1"
/bc.xref="GI:4210971"
/translation="MPRAPRCRAKELLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVL"
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Homo sapiens telomerase reverse transcriptase (TERT) gene, partial
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1. (bases 1 to 15332)

Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Hann, S.R., Adams, R.R., Lichtsteiner, S., Chin, L., Morin, G.B. and DePinho, R.A.

Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation oncogene 18 (5), 1219-1226 (1999)

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10022128
                                                     McMaster University, 1200 Main
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join(3997. .4215,4320. .>4356)
/gene="TERT"
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100.0%; Pred. No. 2.4e-29;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                    , ....(<3997. .4215,4320. .>4356)
2 (bases 1 to 4356)
Cong, Y.S., Wen, J. and Bacchetti, S.
Direct Submission
Submitted (05-0CT-1998) Pathology, Mc
St. W., Hamilton, ON LBN 325, Canada
Location/Qualifiers
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                                                                                                                                                                                             1. .>4356
/gene="TERT"
1. .3996
/gene="TERT"
join(<3997. .4
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Homo sapiens
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Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
AF007365
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                           1657 GAGTITCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCC 1716
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Cong Y.S., Wan, J. and Bacchetti, S.
The human telomerase catalytic subunit hTERT: organization of the gene and characterization of the promoter
Hum. Mol. Genet. 8 (1), 137-142 (1999)
9897342
     182 GAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCC 241
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 4321)

Morin,G.B. and Andrews,W.H.

Promoter for telomerase reverse transcriptase
Patent: US 6610839-A 6 26-AUG-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%; Score 244; DB 6; I
100.0%; Pred. No. 2.4e-29;
ive 0; Mismatches 0;
                                                                                                                                                                                                  DNA
                                                                                                                                                                                               AR390473 4321 bp
Sequence 6 from patent US 6610839.
AR390473
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                  AR390473.1 GI:40112397
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Best Local Similarity 100.
Matches 244; Conservative
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13438 GAGTTTCAGGCAGCCCTGCGTCCTGCTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCC 13497
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RPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFIGSRPWMPGTPRRLPRLPRLPGRYWQWRPL
FLELIGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQ
LLRQHSSPWQYYGFYRACLRRLVPPGLWGSRHNBRRFLRNTKKFISLGKHAKLSLQEL
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                                                                                                                                                                                                                                                                                                                                                                                                     /product="telomerase reverse transcriptase"
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/fb xref="GI:4580663"
/translation="MPRAPRCRYRSLIRSHYREVLPLATFVRRLGPQGWRLVQRGDPARRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGARNVLAFGFALDGARGGPPEAFTSYRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV
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2 (bases 1 to 15332)
Morin,G.B., Carlos,R. and Adams,R.R.
Direct Submission
Submitted (2.1-JNN-1999) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCTCCTCCGCGCGGGGCCCCCGTCCCGACCCCTCCCGGGGTCCCCGGCCCAGCCCC 121
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join(13602. .13720,13825. .>15178)
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1 (bases 1 to 15418)
10(301d,J.D. and Lebkowski,J.S.
Methods for providing differentiated stem cells
                                                                                                                                                                                                                                 1. .13466
/gene="TERT"
join(13447. .13720,13825. .>15178)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%; Score 244; DB 9; L
llarity 100.0%; Pred. No. 1.5e-29;
Conservative 0; Mismatches 0;
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                                                                                                               1. 15332
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/organism="Homo sapiens"
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1. .>15332
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Matches 244;
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                                                                              Length 15418;
                                                                                                   0; Indels
                                                                            99.6%; Score 244; DB 6; I
llarity 100.0%; Pred. No. 1.5e-29;
Conservative 0; Mismatches 0;
Patent: US 6576464-A 1 10-JUN-2003;
Location/Qualifiers
1 .15418
/organism="unknown"
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                                                                                        Similarity
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-932-581-24
US-10-338-294-24
US-10-863-075-24
US-10-140-763A-12
US-10-140-969-17
US-10-840-455-1
US-09-932-581-25
US-10-388-294-25
US-10-840-455-3
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          5615251 segs, 3030001701 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Maximum DB E
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                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                            Run on:
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## ALIGNMENTS

US-10-081-969-94
Sequence 94, Application US/10081969
| Sequence 94, Application No. US20030104625A1
| Septence 94, Application No. US20030104625A1
| Septence 94, Application No. US20030104625A1
| Septence No. US20030104625A1
| APPLICANT: Chengly, Sheila APPLICANT: Connelly, Sheila APPLICANT: Enniet, David APPLICANT: Enniet, David APPLICANT: Hallenbeck, Paul APPLICANT: Hallenbeck, Paul APPLICANT: Macko, Michael APPLICANT: Macko, Michael APPLICANT: Macko, Michael APPLICANT: Netword, David APPLICANT: Police, Seshidhar APPLICANT: Police, Seshidhar APPLICANT: Professor Netword, David APPLICANT: Steward, David APPLICANTON NUMBER: US 60/270, 922
| PRIOR FILING DATE: 2001-06-01

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GENERAL INCORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Fraser, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Praser, Stephanie
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
CURRENT APPLICATION NUMBER: US/10/336,294
CURRENT FILING DATE: 2003-01-07
PRIOR PAPLICATION NUMBER: US/09/932,581
PRIOR PELING DATE: 2000-08-17
PRIOR PELING DATE: 2000-08-17
PRIOR PELING DATE: 2000-09-01
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                                 1 ccccacgrescesascressascressescresserectescrerreactrescrerreascr
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                                                                                                                                              CGAGTTTCAGGCAGGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC
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100.0%; Pred. No. 7.1e-51;
tive 0; Mismatches 0;
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US-10-863-075-24
Sequence 24, Application US/10863075
Publication No. US2050059622A1
GENERAL INFORMATION:
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; Publication No. US20030171326A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 245; Conservative
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; ORGANISM: human
US-10-338-294-24
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US-09-332-581-24
i Sequence 24, Application US/09932581
i Sequence 24, Application US/09932581
i Publication No. US20030050264A1
i GENERAL INFORMATION:
i APPLICANT: Andrews, William H.
i APPLICANT: Fraser, Christopher A.
i APPLICANT: Fraser, Stephanie
i APPLICANT: Fraser, Stephanie
i TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
i TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
i TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
i TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
i TITLE OF INVENTION: TELOMOSEASE (TERT) EXPRESSION
i TITLE OF INVENTION: TELOMOSEASE (TERT)
i PRIOR PELICATION NUMBER: 60/230,174
i PRIOR PILING DATE: 2000-09-01
i PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 245; DB 15; Length 245; 100.0%; Pred. No. 7.2e-51; cive 0; Mismatches 0; Indels 0
                                                                       FEATURE:
NAME/KEY: promoter
LOCATION: 1)..(245)
COTHER INFORMATION: A 245 bp fragment of the hTERT promoter
US-10-081-969-94
                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Matches 245; Conservative
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Best Local Similarity 100.
Matches 245; Conservative
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US-09-932-581-24
TYPE: DNA
ORGANISM: Human
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LENGTH: 261
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Gaps

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194 CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACCC 253 181 CGAGTITCAGGCAGCGCTGCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGGCCACCC

240

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61 CCGCCTCCTCCGCGCGGGACCCCGGCCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC 120
                                                                                                                                                                                                                                                                                                                    181 CGAGTITCAGGCAGCGCTGCTGCTGCTGCACGTGGGAAGCCCTGGCCCCGGGCCACCC 240
                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(955)
CTHER INFORMATION: Fig.47. Sequence of the right end of Arl?pAE2fFTrtex
US-10-081-969-17
                                                                      36 CCCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCTTCACCTTCCAGCT
                                                                                                                                                              96 CCGCCTCCTCCGCGCGCGCCCGCCCGTCCCGACCCCTCCCGGGTCCCCGGGCCCC
                                                                                                                                                                                                                                                         156 CCTCCGGGCCCTCCCACCCCTTCCTTTCCGCGGCCCCCCTCTCTCCTCGCGGG
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Gaps
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TITLE OF INVENTION: No. US20030104625Alel Oncolytic Adenoviral Vectors
FILE REFERENCE: 4-31704A/GII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 245; DB 15; Length 955; Best Local Similarity 100.0%; Pred. No. 4.9e-51; Matches 245; Conservative 0; Mismatches 0; Indels 0
  0; Indels
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/270,922
PRIOR FILING DATE: 2001-02-3
PRIOR APPLICATION NUMBER: US 60/295,037
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 17
LENGTH: 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/081,969
CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Viral vector sequence
                                                                                                                                                                                                                                                                                                                                                             216 CGAGTTTCAGGCAGCGCTGCGTCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cheng, Cheng
APPLICANT: Clarke, Lori
APPLICANT: Connelly, Shella
APPLICANT: Ennist, David
APPLICANT: Forry-Schaudies, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/10081969
Publication No. US20030104625A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hay, Carl, John
Jakubczak, John
Kaleko, Michael
Phipps, Sandrina
Police, Sashidhar
Ryan, Petricia
Steward, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Hallenbeck, Paul
    245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              CCGCG 245
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                                                          APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/863,075
CURRENT FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR APPLICATION NUMBER: 60/230,345
PRIOR FILING DATE: 2000-010-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 240
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TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression
FITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression
FILE REPERENCE: SIER-012
CURRENT APPLICATION NUMBER: US/10/140,763A
CURRENT PILING DATE: 2002-05-07
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 245; DB 19;
; Pred. No. 7.1e-51;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10140763A Publication No. US20030104420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: oligonucleotide US-10-140-763A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.
Matches 245; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 CCGCG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: human
US-10-863-075-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-140-763A-12
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241 CCGCG 245
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Sequence 1, Application US/10840455

Publication No. US20050032094A1

GENERAL INFORMATION:

APPLICANT: Bayer Aktiengesellschaft

APPLICANT: Hagen, Gustav

APPLICANT: Wick, Maresa

APPLICANT: Wick, Maresa

APPLICANT: APPLICANT: APPLICANT: CONTROW MARES

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

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TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

TITLE OF INVENTION: Regulatory DNA Sequences

FRIOR FILING DATE: 1097-12-22

PRIOR FILING DATE: 1097-12-22

PRIOR FILING DATE: 1097-12-24

PRIOR FILING DATE: 1097-12-14

PRIOR FILING DATE: 1097-14-14

PRIOR FILING DATE: 1097-12-14

PRIOR FILING DATE: 1097-
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                                                                                                                                                                                  CGAGTTTCAGGCAGCGCTGCGTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCC 240
500 CCCCACGIGGCGGAGGGACTGGGGACCCGGGCACCCGTCCTGCCCCTTCACCTTCCAGCT 441
                                                                                               380 CCTCCGGGCCCTCCCAGCCCCTCCCTTTCCGCGGCCCCGCCTCTCTCGCGGGC 321
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Best Local Similarity 100.
Matches 245; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CCGCG 245
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RESULT 8

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APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
APPLICANT: Fraser, Stephanie
TITLE OF INVENTION: MCHAMBASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REPERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/09/932,581
PRIOR APPLICATION NUMBER: US/09/932,581
PRIOR APPLICATION NUMBER: 06/227,865
PRIOR PILING DATE: 2000-08-17
PRIOR PLING DATE: 2000-08-24
PRIOR PLING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 5228
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| Publication No. US20030171326A1
| Publication No. US20030171326A1
| GENERAL INFORMATION:
| APPLICANT: Andrews, William H.
| APPLICANT: Foster, Christopher A.
| APPLICANT: Fraser, Stephanie
| APPLICANT: MCHATION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
| TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT)
| FILE REPERENCE: SIER-005
| CURRENT APPLICATION NUMBER: US/09/932,581
| PRIOR APPLICATION NUMBER: (SO/227,865)
| PRIOR FILING DATE: 2000-08-24
| PRIOR APPLICATION NUMBER: 60/230,174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCGCCTCCTCCGCGCGCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCCAGCCC 120
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100.0%; Pred. No. 2.9e-51;
tive 0; Mismatches 0;
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Sequence 25, Application US/09932581 Publication No. US20030050264A1 GENERAL INFORMATION: APPLICANT: Andrews, William H.
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.7
Matches 245; Conservative
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11269 CCGCG 11273
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US-10-863-075-25

Sequence 25, Application US/10863075

Publication No. US20050059622A1

GENERAL INFORMATION:
APPLICANT: Fraders, William H.
APPLICANT: Frader, Christopher A.
APPLICANT: Praser, Stephanie
APPLICANT: Mohammadpour, Hamid
ITILE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
ITILE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
ITILE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
ITILE OF INVENTION: UNUMBER: US/10/863,075
CURRENT APPLICATION NUMBER: US/10/863,075
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
SEQ ID NOS: 25

UNUMBER OF SEQ ID NOS: 25

LENGTHARE: FRASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                             Query Match 100.0%; Score 245; DB 16; Best Local Similarity 100.0%; Pred. No. 2.9e-51; Matches 245; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

OTHER INFORMATION: synthetic expression plasmid
US-10-863-075-25
                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic expression plasmid US-10-338-294-25
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 5928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 3, Application US/10840455
; Sequence 3, Application WS/10840455
; Publication No. U920050032094A1
; GENERAL INFORMATION:
    APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustev
; APPLICANT: Wick, Maresa
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: LoA 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT APPLICATION NUMBER: US/10/8216
; PRIOR FILING DATE: 1998-12-22
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 2000-09-21
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3.2
; ERNCEN . 13.3.2
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                                                                                                                                                                                                                   231 CGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACC 290
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121 corceasecerecenses accerecerrecerres as a corcease en 180
                                                                                                                         171 CCTCCGGGCCCTCCCAGCCCCTCCCTTTCCGCGGCCCCGCCCTCTCCTCGCGGCG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ccaccrccrccacaccccaccccarcccancccrcccagarcccrccagarcc
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100.0%; Pred. No. 2.5e-51;
tive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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NAME/KEY: exon
LOCATION: (1) ... (11492)
LOCATION: (1) ... (11492)
NAME/KEY: intron
LOCATION: (11493) ... (11596)
OTHER INFORMATION: intron 1
NAME/KEY: exon
LOCATION: (11597) ... (12950)
OTHER INFORMATION: intron 2
NAME/KEY: intron
LOCATION: (12951) ... (21566)
OTHER INFORMATION: intron 2
NAME/KEY: exon
LOCATION: (21567) ... (21762)
OTHER INFORMATION: intron 3
NAME/KEY: intron
LOCATION: (2163) ... (24032)
OTHER INFORMATION: intron 3
NAME/KEY: intron
LOCATION: (24033) ... (24199)
OTHER INFORMATION: intron 4
NAME/KEY: intron
LOCATION: (24033) ... (24899)
OTHER INFORMATION: intron 4
NAME/KEY: intron
LOCATION: (24000) ... (25393)
OTHER INFORMATION: intron 5
NAME/KEY: intron
LOCATION: (24000) ... (25549)
OTHER INFORMATION: intron 5
NAME/KEY: intron
LOCATION: (25394) ... (25549)
OTHER INFORMATION: exon 6
LOCATION: (25550) ... (30196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: (30195)...(30292)
OTHER INFORMATION: exon 7
NAME/KEY: intron
LOCATION: (30293)...(31272)
OTHER INFORMATION: intron 7
NAME/KEY: exon
LOCATION: (31273)...(31369)
OTHER INFORMATION: exon 8
NAME/KEY: intron
LOCATION: (31399)...(33843)
OTHER INFORMATION: intron 8
NAME/KEY: intron
LOCATION: (31369)...(33843)
OTHER INFORMATION: intron 8
NAME/KEY: unanure
LOCATION: 31460
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LOCATION: (33844)...(33957)
OTHER INFORMATION: exon 9
NAME/KEY: intron
LOCATION: (33958)...(35941)
OTHER INFORMATION: intron 9
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LOCATION: (36014)...(37884)
OTHER INFORMATION: intron 10
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OTHER INFORMATION: intron 11
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LOCATION: (37885)...(38073)
OTHER INFORMATION: exon 11
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LOCATION: (35942)...(36013)
OTHER INFORMATION: exon 10
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LOCATION: (41875)...(42001)
OTHER INFORMATION: exon 12
Sequence 43, Application US/10840455
; Sequence 43, Application US/10840455
; Sequence 43, Application US/10840455
; Publication No. US20050032094a1
; GENERAL INFORMATION:
    APPLICANT: Bayer Aktiengesellschaft
    APPLICANT: Bayer Aktiengesellschaft
    APPLICANT: Wick, Maresa
    APPLICANT: Wick, Maresa
    APPLICANT: Wick, Maresa
    TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
    TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
    TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
    TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
    CURRENT APPLICATION NUMBER: US/10/840,455
    CURRENT FILING DATE: 1998-12-22
    PRIOR PELLING DATE: 1998-12-22
    PRIOR PELLING DATE: 1999-12-22
    PRIOR APPLICATION NUMBER: DE19757984.1
    PRIOR FILING DATE: 1997-12-24
    PRIOR FILING DATE: 1997-12-24
    SOFTWARE: PatentIn version 3.2
    SEQ ID NO 43
    LENGTH: 26414
    Type: Nan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 245; DB 19; Length 26414; Best Local Similarity 100.0%; Pred. No. 1.9e-51; Matches 245; Conservative 0; Mismatches 0; Indels 0;
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Patent No. US20020045588A1

GRUERAL INFORMATION:

APPLICANT: William Gaarde

APPLICANT: William Gaarde

APPLICANT: Wannia

APPLICANT: William Garde

TITLE OF INVENTION:

FILE REFERENCE: ISPH-0527

CURRENT APPLICATION NUMBER: US/09/733,294A

CURRENT FILIG DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-05-16

WUMBER OF SEQ ID NOS: 108

SEQ ID NO 30

LENGTH: 51552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-733-294A-30
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291

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Sequence 1, Application US/10212667
; Publication No. US20030082722A1
; General INFORMATION:
GAPLICANT: FANG BIANGLIANG
; TITLE OF INVENTION: METHOD FOR AMPLIFYING EXPRESSION FROM A CELL SPECIFIC
; TITLE OF INVENTION: PROMOTER
; TITLE OF INVENTION: PROMOTER
; TITLE OF INVENTION: PROMOTER
; CURRENT APPLICATION NUMBER: US/10/212,667
; CURRENT APPLICATION NUMBER: 06/310,905
; PRIOR APPLICATION NUMBER: 60/310,905
; RIOR APPLICATION NUMBER: 60/310,905
; ROFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH:: 378
                                                                                                                                                                                                                                                                                                                                    112 CGCCTCCTCCGCGGGGGGCCCCGCCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCC 171
                                                                                                                                                                                                                                        52 CCCACGTGGCGGAGGGACTGGGGACCCGGCCATCCTCCCTTCCAGCTC 111
                                                                                                                                                                                                                                                                                                       62 GGCTCCTCCGCGGGGCCCCGCCCGGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGGCCACCCC 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                 232 GAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: Primer US-10-212-667-1
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                                                                                                                      Length 298;
                                                                                                                                                                  Indels
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                                                                                                                                                                                                              2 CCCACGTGGCGGAGGGACTGGGGACCCGGGCACCCGTCC
                                                                                                               Query Match
99.6%; Score 244; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 244; Conservative 0; Mismatches 0;
; ORGANISM: Homo sapiens
; PEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 CGCG 245
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| Sequence 17. Application US/10674836
| Publication No. US20040072787A1
| GENERAL INFORMATION:
| APPLICANT: Morin, Greeg B.G.
| APPLICANT: Lichtsteiner, Serge
| APPLICANT: Vasserot, Alain
| APPLICANT: Adams, Robert R.
| APPLICANT: Geron Corporation
| TITLE OF INVENTION: Regulatory Sequences and Methods of Using
| TITLE OF INVENTION NUMBER: US/10/674,836
| CURRENT FILING DATE: 1030-09-29
| PRIOR FILING DATE: 1999-02-04
| NUMBER OF SEQ ID NOS: 23
| SOFTHARE: PatentIn Ver. 2.1
| SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COGCCTCCTCCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCCGGCCCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 245; DB 9; Length 51552; Best Local Similarity 100.0%; Pred. No. 1.6e-51; Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: (46130) ...(46254)
OTHER INFORMATION: exon 14
NAME/KEY: intron
LOCATION: (46255) ...(47035)
OTHER INFORMATION: intron 14
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: intron 14
NAME/KEY: exon
LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
                                                                                                                                     NAME/KEY: intron
LOCATION: (42944)...(46129)
OTHER INFORMATION: intron 13
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
                     LOCATION: (42002)...(42881)
OTHER INFORMATION: intron 12
                                                                                         LOCATION: (42882)...(42943)
OTHER INFORMATION: exon 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
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